

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:24:27 ; Search time 12.1667 Seconds

(without alignments)
631.182 Million cell updates/sec

Title: US-09-931-186-20

Perfect score: 1304

Sequence: 1 MAACRSVAGLVAVITGAS.....ENPFLNGEVRIDGAIKMP 261

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database :

1: Issued Patents AA: *
2: /cgn2_6/pdata/1/aa/5A.COMB.pep: *
3: /cgn2_6/pdata/1/aa/5B.COMB.pep: *
4: /cgn2_6/pdata/1/aa/5A.COMB.pep: *
5: /cgn2_6/pdata/1/aa/5B.COMB.pep: *
6: /cgn2_6/pdata/1/aa/PCITUS.COMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1300	99.7	261	4	US-08-815-225-2
2	1300	99.7	261	4	US-08-815-225-3
3	1300	99.7	261	4	US-09-347-878-50
4	666.5	51.1	388	4	US-08-980-832-41
5	328.5	25.2	243	4	US-09-239-052-2
6	302	23.2	255	4	US-08-815-225-4
7	300.5	23.0	333	1	US-08-815-225-4
8	298	22.9	263	4	US-09-134-001C-4512
9	296.5	22.7	262	4	US-09-134-001C-4512
10	294	22.5	315	3	US-09-563-189B-6
11	294	22.5	315	3	US-08-793-035-9
12	287.5	22.0	244	1	US-08-793-035-10
13	287.5	22.0	244	1	US-08-793-035-10
14	287.5	22.0	244	2	US-08-562-14B-13
15	287.5	22.0	244	4	US-08-729-594A-13
16	287.5	22.0	244	4	US-08-937-993-13
17	287.5	22.0	246	6	5512669-4
18	287.5	22.0	273	6	5529279-7
19	275.5	21.1	274	4	US-09-134-001C-4431
20	271.5	20.8	246	3	US-09-134-001C-4825
21	271.5	20.8	246	4	US-09-238-481-2
22	269	20.6	231	4	US-09-572-810A-2
23	268.5	20.6	337	1	US-08-440-856A-3
24	267	20.5	186	4	US-08-858-207A-270
25	267	20.5	256	4	US-09-504-358-14
26	267	20.5	256	4	US-09-954-314-14
27	266	20.4	247	1	US-08-241-766-13

28	258	19.8	261	4	US-09-468-738A-29	Sequence 29, Appl
29	258	19.8	261	4	US-09-940-019-29	Sequence 29, Appl
30	255.5	19.6	263	6	5529279-4	Patent No. 5529279
31	253.5	19.4	263	4	US-09-134-001C-3505	Sequence 3505, Ap
32	252.5	19.4	257	4	US-09-134-001C-3562	Sequence 3562, Ap
33	251.5	19.3	252	3	US-08-822-332-8	Sequence 8, Appl
34	251.5	19.3	252	3	US-09-466-109-8	Sequence 8, Appl
35	246	18.9	256	1	US-08-559-808B-7	Sequence 8, Appl
36	243	18.6	271	2	US-07-637-885-2	Sequence 2, Appl
37	243	18.6	359	1	US-08-440-856A-8	Sequence 2, Appl
38	240	18.4	258	4	US-09-504-358-12	Sequence 12, Appl
39	240	18.4	258	4	US-09-954-314-12	Sequence 12, Appl
40	240	18.4	292	3	US-09-109-205-2	Sequence 2, Appl
41	240	18.4	292	3	US-09-443-184-8	Sequence 58, Appl
42	231.5	17.8	251	3	US-08-822-332-9	Sequence 9, Appl
43	231.5	17.8	251	3	US-09-466-109-9	Sequence 9, Appl
44	225	17.3	283	4	US-09-367-012-1	Sequence 1, Appl
45	225	17.3	283	4	US-09-777-157A-1	Sequence 5042, Ap
46	216	16.6	267	4	US-09-134-001C-5042	Sequence 5346, Ap
47	211	16.2	283	4	US-09-134-001C-5346	Sequence 9, Appl
48	208	16.0	313	4	US-09-413-814-8	Sequence 4339, Ap
49	207	15.9	290	4	US-09-134-001C-4339	Sequence 2, Appl
50	204	15.6	248	2	US-09-099-367-2	Sequence 11, Appl
51	189	14.5	248	4	US-09-385-028-11	Sequence 2, Appl
52	186.5	14.3	292	4	US-09-468-738A-2	Sequence 2, Appl
53	186.5	14.3	292	4	US-09-940-019-2	Sequence 5, Appl
54	186.5	14.3	296	3	US-09-002-298-5	Sequence 23, Appl
55	186.5	14.3	296	4	US-09-468-738A-23	Sequence 39, Appl
56	186.5	14.3	296	4	US-09-940-019-23	Sequence 39, Appl
57	186.5	14.3	318	4	US-08-729-554A-39	Sequence 39, Appl
58	186.5	14.3	318	4	US-08-937-993-39	Sequence 2664, Ap
59	185	14.2	244	1	US-08-762-129-4	Sequence 4059, Ap
60	182.5	14.0	272	4	US-09-134-001C-2864	Sequence 2, Appl
61	182.5	14.0	295	4	US-09-134-001C-4059	Sequence 3, Appl
62	182	14.0	244	1	US-08-762-129-3	Sequence 2, Appl
63	182	14.0	257	4	US-09-287-097-2	Sequence 2, Appl
64	182	14.0	295	4	US-09-026-482B-2	Sequence 15, Appl
65	181.5	13.9	318	2	US-08-562-114B-15	Sequence 15, Appl
66	181.5	13.9	318	3	US-09-109-205-15	Sequence 15, Appl
67	181.5	13.9	318	4	US-08-729-554A-15	Sequence 1, Appl
68	181.5	13.9	318	4	US-09-880-427-1	Sequence 1, Appl
69	181.5	13.9	318	4	US-09-306-538B-1	Sequence 1, Appl
70	181.5	13.9	318	4	US-08-937-993-15	Sequence 15, Appl
71	180.5	13.8	318	4	US-08-375-962B-14	Sequence 1, Appl
72	180.5	13.8	318	4	US-08-940-424-3	Sequence 3, Appl
73	175.5	13.5	244	1	US-08-762-129-1	Sequence 38, Appl
74	174	13.3	318	4	US-08-729-554A-38	Sequence 98, Appl
75	174	13.3	301	4	US-08-937-993-38	Sequence 1, Appl
76	173	13.3	301	4	US-09-288-143-98	Sequence 37, Appl
77	172	13.2	303	3	US-09-002-288-1	Sequence 37, Appl
78	166.5	12.8	317	4	US-08-729-554A-37	Sequence 21, Appl
79	166.5	12.8	317	4	US-08-937-993-37	Sequence 21, Appl
80	162	12.4	255	4	US-09-036-967A-21	Sequence 1, Appl
81	162	12.4	255	4	US-09-370-700-21	Sequence 1, Appl
82	161.5	12.4	319	2	US-08-937-993-37	Sequence 1, Appl
83	161.5	12.4	319	2	US-09-195-021-1	Sequence 1, Appl
84	160.5	12.3	317	3	US-09-109-205-18	Sequence 5, Appl
85	160.5	12.3	317	3	US-08-940-424-5	Sequence 2, Appl
86	160.5	12.3	360	4	US-09-740-028A-2	Sequence 7, Appl
87	159.5	12.2	274	4	US-09-740-028A-4	Sequence 36, Appl
88	159.5	12.2	335	3	US-09-002-298-7	Sequence 36, Appl
89	158.5	12.0	316	4	US-08-940-424-2	Sequence 6, Appl
90	156.5	12.0	316	4	US-08-729-554A-36	Sequence 19, Appl
91	156.5	12.0	316	4	US-08-937-993-36	Sequence 3, Appl
92	156.5	12.0	335	3	US-09-002-298-6	Sequence 3, Appl
93	156.5	11.8	335	3	US-09-109-205-19	Sequence 3, Appl
94	152.5	11.7	317	2	US-08-977-847-3	Sequence 3, Appl
95	152.5	11.7	317	2	US-09-195-021-3	Sequence 3, Appl
96	152.5	11.7	317	4	US-08-940-424-4	Sequence 39, Ap
97	152	11.7	318	4	US-09-605-785-339	Sequence 39, Ap
98	152	11.7	318	4	US-09-439-313-339	Sequence 39, Ap
99	152	11.7	318	4	US-09-352-616A-339	Sequence 12, Appl
100	151	11.6	327	1	US-08-375-962B-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-08-815-225-2Sequence 2, Application US/08815225
Patent No. 6268479

GENERAL INFORMATION:

APPLICANT: Stern, David M.

APPLICANT: Yan, Shi Du

TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE

TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING

TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/815,225

FILING DATE: 12-MAR-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/55209

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-815-225-2

Query Match 99.7%; Score 1300; DB 4; Length 261;

Best Local Similarity 99.6%; Pred. No. 4.7e-136;

Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MAACRSYKGLVAVITGGASGLGATAEKLVGQASAVLLDLPNSGGGAQAKKLNKCVF 60
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DB 1 MAACRSYKGLVAVITGGASGLGATAEKLVGQASAVLLDLPNSGGGAQAKKLNKCVF 60
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QY 61 APADVTSEKDVOTALAKGKFRGVDAVAVNCAGIAVASKTYNLKKGQTHLEDFORVLDV 120
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DB 61 APADVTSEKDVOTALAKGKFRGVDAVAVNCAGIAVASKTYNLKKGQTHLEDFORVLDV 120
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QY 121 NLMGTFNIVRLVAGKGNPDGQGRGVITNTASVAAPFEGVQGAASASKGGIVGNTL 180
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QY 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKYNFLASQVFPFRLGDPAEYAHVQAI 240
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DB 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKYNFLASQVFPFRLGDPAEYAHVQAI 240
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QY 241 IENPFLNGEVIRLDGAIRMOP 261
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DB 241 IENPFLNGEVIRLDGAIRMOP 261
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RESULT 2

US-08-815-225-3

Sequence 3, Application US/08815225

Patent No. 6268479

GENERAL INFORMATION:

APPLICANT: Stern, David M.

APPLICANT: Yan, Shi Du

TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE

TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING

TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/815,225

FILING DATE: 12-MAR-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/55209

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-815-225-3

Query Match 99.7%; Score 1300; DB 4; Length 261;

Best Local Similarity 99.6%; Pred. No. 4.7e-136;

Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 61 APADVTSEKDVOTALAKGKFRGVDAVAVNCAGIAVASKTYNLKKGQTHLEDFORVLDV 120
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DB 121 NLMGTFNIVRLVAGKGNPDGQGRGVITNTASVAAPFEGVQGAASASKGGIVGNTL 180
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QY 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKYNFLASQVFPFRLGDPAEYAHVQAI 240
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DB 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKYNFLASQVFPFRLGDPAEYAHVQAI 240
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QY 241 IENPFLNGEVIRLDGAIRMOP 261
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DB 241 IENPFLNGEVIRLDGAIRMOP 261
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RESULT 3

US-09-347-878-50

Sequence 50, Application US/09347878C

Patent No. 6376210

GENERAL INFORMATION:

APPLICANT: Yuan, Chong

;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
;; FILE REFERENCE: 25885-1651
;; CURRENT APPLICATION NUMBER: US/09/347,878C
;; CURRENT FILING DATE: 1999-07-06
;; NUMBER OF SEQ ID NOS: 75
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 50
;; LENGTH: 261
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-347-878-50

Query Match 99.7%; Score 1300; DB 4; Length 261;
Best Local Similarity 99.6%; Pred. No. 4.7e-136;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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1 MAAACRSVKGLVAVITGGASGLGATAEERLVGGASAVLLDLPNSGGEAOKKLNVCYF 60
Db 1 MAAACRSVKGLVAVITGGASGLGATAEERLVGGASAVLLDLPNSGGEAOKKLNVCYF 60
QY 61 APADVTSEKDVQALALAKGFGVAVVAVNCAGIAVASKTYNKKQOTHTLEDFORVLDV 120
61 APADVTSEKDVQALALAKGFGVAVVAVNCAGIAVASKTYNKKQOTHTLEDFORVLDV 120
Db 61 APADVTSEKDVQALALAKGFGVAVVAVNCAGIAVASKTYNKKQOTHTLEDFORVLDV 120
QY 121 NLGTFENVIRLVAGEMQNEPDGQGRGVIIINTASVAAREGQVQAAYSASKGIYGMTL 180
121 NLGTFENVIRLVAGEMQNEPDGQGRGVIIINTASVAAREGQVQAAYSASKGIYGMTL 180
Db 121 NLGTFENVIRLVAGEMQNEPDGQGRGVIIINTASVAAREGQVQAAYSASKGIYGMTL 180
QY 181 PIADLAPIGIRVWTIAPGLFGPPLTSLPEKYNFLASQVPPPSRLGDAEYAHVQAI 240
181 PIADLAPIGIRVWTIAPGLFGPPLTSLPEKYNFLASQVPPPSRLGDAEYAHVQAI 240
Db 181 PIADLAPIGIRVWTIAPGLFGPPLTSLPEKYNFLASQVPPPSRLGDAEYAHVQAI 240
QY 241 IENPFLNGEYIRLDGAIRMQP 261
241 IENPFLNGEYIRLDGAIRMQP 261
Db 241 IENPFLNGEYIRLDGAIRMQP 261

RESULT 4
US-08-980-832-41
; Sequence 41, Application US/08980832B
; Patent No. 6291204
; GENERAL INFORMATION:
; APPLICANT: Pasamontes, Luis
; APPLICANT: Tsygankov, Yuri
; TITLE OF INVENTION: Improved Fermentative Carotenoid Production
; FILE REFERENCE: Improved Fermentative Carotenoid
; CURRENT APPLICATION NUMBER: US/08/980,832B
; CURRENT FILING DATE: 1997-12-01
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Flavobacterium sp. R1534
US-08-980-832-41

Query Match 51.1%; Score 666.5; DB 4; Length 388;
Best Local Similarity 55.5%; Pred. No. 1.7e-65;
Matches 14; Conservative 35; Mismatches 69; Indels 9; Gaps 3;

QY 8 VKGLVAVITGGASGLGATAEERLVGGASAVLLDLPNSGGEAOKKLNVCYFAPADYVS 67
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Db 143 IEGRVFVVTGAASGLGASARMLAOGGAKVYIADL-----AEPKDAPEGAVHAACDVID 196
143 IEGRVFVVTGAASGLGASARMLAOGGAKVYIADL-----AEPKDAPEGAVHAACDVID 196
QY 68 EKDVQTLALAKGFGVAVVAVNCAGIAVASKTYNKKQOTHTLEDFORVLDVNLGTFNV 127
68 EKDVQTLALAKGFGVAVVAVNCAGIAVASKTYNKKQOTHTLEDFORVLDVNLGTFNV 127
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197 ATAQOTAIATATREFGLDLYNCAGIAPAEERM--IGRDPPHLDSPARAVTINLIGSEFN 254
QY 128 VIRLVAGEMQNEPDGQGRGVIIINTASVAAREGQVQAAYSASKGIYGMTLPIARDLA 187
128 VIRLVAGEMQNEPDGQGRGVIIINTASVAAREGQVQAAYSASKGIYGMTLPIARDLA 187
Db 255 MARLAARMAARNEVYR-GERGVIVNTASIAADQDQICQAVAYASKSGVAGNTLPIARDLA 313
255 MARLAARMAARNEVYR-GERGVIVNTASIAADQDQICQAVAYASKSGVAGNTLPIARDLA 313
QY 188 PIGIRVWTIAPGLFGPPLTSLPEKYNFLASQVPPPSRLGDAEYAHVQAIENPFLN 247
188 PIGIRVWTIAPGLFGPPLTSLPEKYNFLASQVPPPSRLGDAEYAHVQAIENPFLN 247

Db 314 RHGIRVWTIAPGLFGPPLTSLPEKYNFLASQVPPPSRLGDAEYAHVQAIENPFLN 373
314 RHGIRVWTIAPGLFGPPLTSLPEKYNFLASQVPPPSRLGDAEYAHVQAIENPFLN 373
QY 248 GEVIRLDGALRMQP 261
248 GEVIRLDGALRMQP 261
Db 374 GEVIRLDGALRMQP 387
374 GEVIRLDGALRMQP 387

RESULT 5
US-09-239-052-2
; Sequence 2, Application US/09239052
; Patent No. 6346395
; GENERAL INFORMATION:
; APPLICANT: Holmes, David J.
; APPLICANT: Zhong, Yiyi
; APPLICANT: Debouck, Christine
; APPLICANT: Jaworski, Deborah D.
; APPLICANT: Wang, Min
; APPLICANT: Warren, Richard L.
; APPLICANT: Kosmetka, Anna L.
; APPLICANT: McDevitt, Damien
; APPLICANT: Ingraham, Karen A.
; APPLICANT: Chalker, Allison F.
; APPLICANT: So, Chi Young
; APPLICANT: Wallis, Nicola G.
; APPLICANT: Pearson, Stewart C.
; TITLE OF INVENTION: FabsG
; FILE REFERENCE: GM10191
; CURRENT APPLICATION NUMBER: US/09/239,052
; CURRENT FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-239-052-2

Query Match 25.2%; Score 328.5; DB 4; Length 243;
Best Local Similarity 35.1%; Pred. No. 2.5e-28;
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;

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15 ITGGASGLGATAEERLVGGASAVLLDLPNSGGE-----AQAKKLNVCYFAPADYVS 68
Db 10 ITGSSGGLGATAEERLVGGASAVLLDLPNSGGE-----NSRGATSEELLEFSYGRVPIGSDVDF 65
10 ITGSSGGLGATAEERLVGGASAVLLDLPNSGGE-----NSRGATSEELLEFSYGRVPIGSDVDF 65
QY 69 KIVQOTLALAKGFGVAVVAVNCAGIAVASKTYNKKQOTHTLEDFORVLDVNLGTFNV 128
69 KIVQOTLALAKGFGVAVVAVNCAGIAVASKTYNKKQOTHTLEDFORVLDVNLGTFNV 128
Db 66 ADARKMIDQAIADLEGSVDVAVNNAGI--TQDTIMLKM-----TEADFEKYNLNLGAFNM 119
66 ADARKMIDQAIADLEGSVDVAVNNAGI--TQDTIMLKM-----TEADFEKYNLNLGAFNM 119
QY 129 IRLVAGEMQNEPDGQGRGVIIINTASVAAREGQVQAAYSASKGIYGMTLPIARDLA 188
129 IRLVAGEMQNEPDGQGRGVIIINTASVAAREGQVQAAYSASKGIYGMTLPIARDLA 188
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120 TQSVL-----KPMKARREGATINNSVYGLMGNIGQANYAASKGLIGTFKSVAREVAS 173
QY 189 IGRVWTIAPGLFGPPLTSLPEKYNFLASQVPPPSRLGDAEYAHVQAIENPFLN 248
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Db 174 KIRRVAVIAPGMIESMRAILSDKIKETIAQIPM-KERGQAEQVADLVFLAGQDYILNG 232
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QY 249 EVIRLDGAIRM 259
249 EVIRLDGAIRM 259
Db 233 QVIAIDGGLSM 243
233 QVIAIDGGLSM 243

RESULT 6
US-08-815-225-4
; Sequence 4, Application US/08815225
; Patent No. 6268479
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE
; TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING
; TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS

Thu Jun 26 06:55:04 2003

us-09-931-186-20.ra1

Page 4

NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,225
FILING DATE: 12-MAR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/55209
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-815-225-4
Query Match 23.2%; Score 302; DB 4; Length 255;
Best Local Similarity 33.6%; Pred. No. 2.3e-25;
Matches 85; Conservative 47; Mismatches 101; Indels 20; Gaps 8;
QY 8 VGLVAVITGASGLGATLAEERLVGGASAVLLDLPNSGGEQAOKKLGNNCFAPADVT 67
DB 4 LSKFTVITIGARGAGLAEARQAVAGARVVLADVLDEGATFARLGDPAARYOHLDTVI 63
QY 68 EKDVQALALAKGKEGRVDVAVNACGIAVASKTYNLKKGOTHTLEDFQRLVDNLMGTEN 127
DB 64 EEWQWYVAVAREFESVDGLVNNAGISTGMFL-----ETESVERFRVVDINLTGVI 117
QY 128 VIRLVAGENGQNEPDGQGVIIINTASVAFAEGGVQAAYSASKSGIVGMLPLIARDIA 187
DB 118 GKMTVIPAM---KDAQG--GSIVNISAAGLMLALTSYGASKGVGSLKLAVALG 171
QY 188 PIGIRMTIAPGLFGPLL--TSLPEKANFLASQVFPFRLG-DPAEVAHYQALIE-- 242
DB 172 TDRIRVNSVHPGFTYPMETGIRGEGENT--PNTPM-GRVNGEGLIAGAVKILSDT 228
QY 243 NPLNGEVIRLDG 255
DB 229 SSYVTGAEIADVG 241
RESULT 7
US-08-440-856A-4
Sequence 4, Application US/08440856A
Patent No. 5750873
GENERAL INFORMATION:
APPLICANT: DELAPORTA, STEPHEN L.
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORSTER
STREET: 2000 PENNSYLVANIA AVE. N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA

ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,856A
FILING DATE: 15-MAY-1995
CLASSIFICATION: 809
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 05463-20001.00
TELEPHONE: (202) 887-1517
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-440-856A-4
Query Match 23.0%; Score 300.5; DB 1; Length 333;
Best Local Similarity 32.5%; Pred. No. 5.2e-25;
Matches 92; Conservative 46; Mismatches 106; Indels 39; Gaps 5;
QY 6 RSYKGLAVITGASGLGATLAEERLVGGASAVLLDLPNSGGEQAOKKLGNNCFAPADY 65
DB 50 KRLGKVAIVTGARGRGGEALVRLFYHGAQVIADDDAGAEALAAAGPHGFCV 109
QY 66 TSEKDVQALALAKGKEGRVDVAVNACGIAVASKTYNLKKGOTHTLEDFQRLVDNLMGT 125
DB 110 SVEEDVERAVRAVARGRDLVLCNNAGV-LGROTRAKKILSFDAEFPRVLRVNAIGA 168
QY 126 FNVIRLVAGENGQNEPDGQGVIIINTASVAFAEGGVQAAYSASKSGIVGMLPLIARD 185
DB 169 ALGKHAHALATQ-----RAGSIIASVAGTGLGSHATASHALVGLTKNAACE 222
QY 186 LAPIGIRMTIAPGLFGPLL-----TSLP-----EKVA 214
DB 223 LGANGIRVNCISPGVATPMLINAMROGHDASTADADADIDDIADVPSQGEYKMEEV 282
QY 215 NPLASQVFPFRLGDPAEVAHYQALIEENPLNGEVIRLDGAI 257
DB 283 RGLATLKGATLRPRDIAE-AALFLASDSKRLISGHNLVVDGV 324
RESULT 8
US-09-134-001C-4512
Sequence 4512, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4512
LENGTH: 263
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4512

Query Match 22.9%; Score 298; DB 4; Length 263;
 Best Local Similarity 32.3%; Pred. No. 6.8e-25;
 Matches 85; Conservative 43; Mismatches 107; Indels 28; Gaps 6;

12 VAVITGGASGIGLATAERLYGOGASAVLLDLPNSGGEAQAQKL---GNCGVAPADVTSE 68
 11 VAVITGGAAGIGLTAERLYGOGASAVLLDLPNSGGEAQAQKL---GNCGVAPADVTSE 70
 69 KDQVATLALAKGKGRVDVAVNCAGIAVASKTYNLKKQGTHTLEDFQRLVDVNLMTFNV 128
 71 DQVSVLNQVVEHGGDLVAVNAGLGMPI-----ESVTPQDFQVGVAVNGVFWG 124
 129 IRLVAGEGONEPDGQGVVILMTASVAFEGQVGOAASASKSGIVGMLTPIARDLAP 188
 125 IOALEOF-----DLGSHGKLIINTSGAGVEGNAGLSYSTKFAVRGLTVQVARDLAE 179
 189 IGRVMTAPGLFGTPLTSLPEKVA-----NFLASQVPPFSRLGDPDAEYAHLY 237
 180 KNITVNAFAPGIVETPMKGIKLAENNOPMEMGKQFTDQIAL-KRLSKPEDVAVNV 238
 238 QAIT--ENPFLNGEVIRLDGAIR 258
 239 SFLASDSDYITGOTIITVDGGR 261

RESULT 9

US-09-363-189B-6
 : Sequence 6, Application US/09363189B
 : Patent No. 6242228
 : GENERAL INFORMATION:
 : APPLICANT: SUGIYAMA, MASAKAZU
 : APPLICANT: TONOCHE, NAOTO
 : APPLICANT: SUZUKI, SHUNICHI
 : APPLICANT: YOKOZAKI, KENZO
 : TITLE OF INVENTION: XYLITOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF
 : FILE REFERENCE: 0010-1024-0
 : CURRENT APPLICATION NUMBER: US/09/363,189B
 : CURRENT FILING DATE: 1999-07-26
 : PRIOR APPLICATION NUMBER: JP10-216047
 : PRIOR FILING DATE: 1998-07-30
 : NUMBER OF SEQ ID NOS: 16
 : SOFTWARE: PatentIn version 3.0
 : SEQ ID NO 6
 : LENGTH: 262
 : TYPE: PRN
 : ORGANISM: Glucobacter oxydans
 : US-09-363-189B-6

Query Match 22.7%; Score 296.5; DB 4; Length 262;
 Best Local Similarity 32.0%; Pred. No. 9.9e-25;
 Matches 87; Conservative 41; Mismatches 109; Indels 35; Gaps 7;

6 RSVKGLVAVITGGASGIGLATAERLYGOGASAVLLDLPNSG---GQAQKKGNNCVFAP 62
 3 KRENGKCVITGGAGNGIGLATAERLYGOGASAVLLDLPNSG---GQAQKKGNNCVFAP 62
 63 ADVTSEKDVQATLALAKGKGRVDVAVNCAGIAVASKTYNLKKQGTHTLEDFQRLVDVNL 122
 63 CDVTSEAVVIGTDSVVRDQKIDLENNAGYOGA---FAPVQDYPSPDFARVLINV 117
 123 MGFNTVIRLVAGEH-GQNEPDQGGQGVVILMTASVAFEGQVGOAASASKSGIVGMLT 181
 118 TGAHVHLKAVSRQMTN-----YGRIVNTASMAVGKPPNKAAGASKGALIALTET 170
 182 IARLAPIGIRVMTAPGLFGTPLTSLPEKVA-----NFLASQVPPFSRLGDPDAEYAHLY 237
 171 AADLAPYNTIRVNAISGNGPFGMEROVELAKVASKYQFSTPPKVVAAQMGISVPM-R 229
 226 RLSDPAEYAHLYQAIT--ENPFLNGEVIRLDG 255
 230 RYGDINETPGVAVFLDGDSSFTMGVNLPIAG 261

RESULT 10

US-08-793-035-9
 : Sequence 9, Application US/08793035
 : Patent No. 6011201

GENERAL INFORMATION:
 APPLICANT: Sladas, Antoni R.
 APPLICANT: White, Andrew
 APPLICANT: Chase, Dianne
 APPLICANT: Elborough, Keiran
 APPLICANT: Fentem, Phillip A.
 TITLE OF INVENTION: B-ketoadyl ACP Reductase Genes From
 TITLE OF INVENTION: Brassica Napus
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: TX
 COUNTRY: US
 ZIP: 77210-4433

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/793,035
 FILING DATE: 28-JUL-1997
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9414622.2
 FILING DATE: 20-JUL-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB95/01678
 FILING DATE: 17-JUL-1995

ATTORNEY/AGENT INFORMATION:
 NAME: Kammerer, Patricia A.
 REGISTRATION NUMBER: 29,775
 REFERENCE/DOCKET NUMBER: MOBT-132
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 713.787.1400
 TELEFAX: 713.787.1440
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 315 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-793-035-9

Query Match 22.5%; Score 294; DB 3; Length 315;
 Best Local Similarity 30.5%; Pred. No. 2.5e-24;
 Matches 80; Conservative 44; Mismatches 116; Indels 22; Gaps 6;

4 ACSRYKGLVAVITGGASGIGLATAERLYGOGASAVLLDLPNSGGEA-----QAQKKGNNC 58
 66 AVPKYVESPVVVTGASRGKRIALSL-CKAGCKTVLVYARAKAEVSGQIEAVGGQA 124
 59 VEPADVTSEKDVQATLALAKGKGRVDVAVNCAGIAVASKTYNLKKQGTHTLEDFQRLV 118
 125 ITFGGVSKAEAVVEMAKTAIDAWGTIDVVVNNAGITRDTLLIRKKSQ-----WDEVI 178
 119 DYNLMGTENVILVAGEGONEPDGQGVVILMTASVAFEGQVGOAASASKSGIVGM 178
 179 DLNLGVFLCTQAKIKMKK-----KRGRIINIASVGLIGNIGNANVAAKAGVIGF 232
 179 TLEIARDLAPIGIRVMTAPGLFGTPLTSLPEKVAANFLASQVPPFSRLGDPDAEYAHLYQ 238
 233 SKTAAREGASRNINNVVCPGFIASDMETAKLGEDMEKKILGTPL-GRYGQEDVAVGLVE 291
 239 AITENP---FNGEVIRLDGAI 257
 292 FLALSPASVITGQAFITDGI 313

RESULT 11
US-08-793-035-10
Sequence 10, Application US/08793035
Patent No. 6011201
GENERAL INFORMATION:
APPLICANT: Slabas, Antoni R.
APPLICANT: White, Andrew
APPLICANT: Chase, Dianne
APPLICANT: Elborough, Kelvin
APPLICANT: Fentem, Phillip A.
TITLE OF INVENTION: B-ketacyl ACP Reductase Genes From
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,035
FILING DATE: 28-JUL-1997
CLASSIFICATION: 890
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9414622.2
FILING DATE: 20-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB95/01678
FILING DATE: 17-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kammerer, Patricia A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: MOBT-132
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713.787.1400
TELEFAX: 713.787.1440
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-793-035-10

Query Match 22.5%; Score 294; DB 3; Length 315;
Best Local Similarity 30.5%; Pred. No. 2.5e-24;
Matches 80; Conservative 44; Mismatches 116; Indels 22; Gaps 6;

DB 4 ACRSVGLVAVITGASGLATLAEKLVGASAVLLDIPNSGGEA-----QAKLGNCC 58
DB 66 AVKVESPVVYVVGASRGISKAIALSL-GRAGCKVLVYARSAKEEVSKEIDVAGQA 124
DB 59 VEPADVTSEKDVOTLALAKGKFGVDVAVNCAIVASKTYNKKGGTHLEDFQRL 118
DB 125 ITFGGVDSKADVDKAMKTRIDAMGTIDVAVNAGITRDLIRMKSQ-----WDEVI 178
DB 119 DVNLMTGFNIRIVAGMGQNEPDGORGVIINTASVAFEGQVQAAYSASRGIVM 178
DB 179 DNLVGFELTQATKIMMK-----BKGRINIISVGLIGNIGQAVYAAKAGVIGF 232
DB 179 TLPIARDLAPIGIRVMTIAGLFGTPLTSLPEKVANFLASQVPPFSRLGPAEYAHVQ 238
DB 233 SKTAARAGASRNINNVVCPGFIASDTAKLGEDMKKITLITPL-GRYGQPDVAVLVE 291
DB 239 AITENP---PLNGEVIRLDGAI 257

DB 292 FLATSPASVITGQAFITDGI 313

RESULT 12
US-08-375-962B-13
Sequence 13, Application US/08375962B
Patent No. 5731195
GENERAL INFORMATION:
APPLICANT: SIMON, ANDRAS; HELLMAN, ULF; WERNSTEDT,
APPLICANT: CHRISTER, ERIKSSON, ULF.
TITLE OF INVENTION: Isolated Nucleic Acid Molecule
TITLE OF INVENTION: Which codes for a 32 kDa Protein Having 11-CIS Retinol
TITLE OF INVENTION: Dehydrogenase Activity, and Which Associates With P63,
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: US
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect (ASCII standard)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,962B
FILING DATE: 20-January-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/258,418
FILING DATE: 6-October-1994
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5372.1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 638-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]
NAME/KEY: reductase (FABG)
US-08-375-962B-13

Query Match 22.0%; Score 287.5; DB 1; Length 244;
Best Local Similarity 29.6%; Pred. No. 8.8e-24;
Matches 75; Conservative 50; Mismatches 113; Indels 15; Gaps 4;

DB 9 KGLVAVITGASGLATLAEKLVGASAVLLDIPNSGGEAQAQKLNCCVFAADVTSE 68
DB 4 EKKILVVGASRGISRAETLAAKGGVIGTATSENGAQISIDANGKGLMLNTDP 63
DB 69 KDVTALALAKGKFGVAVNCAIVASKTYNKKGGTHLEDFQRLDVLNLTGFNV 128
DB 64 ASISEVLKIRAREBEVDILVNNAGITRDLIRMKD-----EDMDIIEFTNLSVERL 117
DB 129 IRLVAGMGQNEPDGGRGVYINTASVAFEGQVQAAYSASRGIVMTLPARDLAP 188
DB 118 SKAVRAMMK-----RHGRITIIIGSVGTMGNGQAVYAAAGLIGFSKSLAREVAS 171
DB 169 IGIRVMTIAPGLFGTPLTSLPEKVANFLASQVPPFSRLGPAEYAHVQ--AITENPFL 246
DB 172 RGIIVNVAPEGFIETDMTRALSDDORAGIQAQV-AGRLGAGQELIANVATLADDEAYI 230

QY 189 IGIKMTIAPGLFETPLTSLPEKYNFLASQVFPFSPRLGDPAEVHLYQ--ATTENPFL 246
DB 172 RGIIVNVVAPGFLETDMTRALSDDOAGILAQVP-AGRLGGAQEIANNVAFLASDEAAVI 230
QY 247 NGEVIRLDGAIRM 259
DB 231 TGETLHVNGMYM 243

RESULT 15
US-08-937-993-13
Sequence 13, Application US/08937993
Patent No. 6399344
GENERAL INFORMATION:
APPLICANT: Eriksson, Ulf; Simon, Andreas; Romert, Anna
TITLE OF INVENTION: ISOLATED PROTEINS HAVING CIS-R
TITLE OF INVENTION: DEHYDROGENASE ACTIVITY
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,993
FILING DATE: September 26, 1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/729,594
FILING DATE: 11-October-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/562,114
FILING DATE: 22-No. 6399344ember-1995
APPLICATION NUMBER: 08/375,962
FILING DATE: 20-January-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/258,418
FILING DATE: 10-June-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6399344man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]reductase
NAME/KEY:
US-08-937-993-13

Query Match 22.0%; Score 287.5; DB 4; Length 244;
Best Local Similarity 29.8%; Pred. No. 8.8e-24;
Matches 75; Conservative 50; Mismatches 113; Indels 15; Gaps 4;

QY 9 KGLVAVITGASGLGATARLYVGOGASAVLLDPPSSGGAGAKKGNKVFAPADVTS 68
DB 4 EGRITAVTGASRGISGRITAEITLARGSKVIGITFSEGAQISIDYLGANGKGLMLVTD 63
QY 69 KDVOTALALAKGFRGVADVAVNCAGIIVASKIYNLKKQTHLEDFQRYLDVNLGTFNV 128

DB 64 ASIESYLEKIRAEFGEDVILVNNAGITRDNLIMRMD-----EEMNDIETNLSVERL 117
QY 129 IRIYAGEMQNEPDGOGGVYIINTASVAAFEQVQAAYSASKGIYGMTPIARDLAP 188
DB 118 SKAVRAMAMRK-----RGRITITGSVGTMGNGQAAVYAAKAGLIFSKISAREVAS 171
QY 189 IGIKMTIAPGLFETPLTSLPEKYNFLASQVFPFSPRLGDPAEVHLYQ--ATTENPFL 246
DB 172 RGIIVNVVAPGFLETDMTRALSDDOAGILAQVP-AGRLGGAQEIANNVAFLASDEAAVI 230
QY 247 NGEVIRLDGAIRM 259
DB 231 TGETLHVNGMYM 243

RESULT 16
5229279-7
Patent No. 5229279
APPLICANT: PEOPLES, OLIVER P.; SINSKEY, ANTHONY J.
TITLE OF INVENTION: METHOD FOR PRODUCING NOVEL POLYESTER
BIOPOLYMERS
NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/556,535
FILING DATE: 13-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 67,695
FILING DATE: 29-AUG-1987
SEQ ID NO: 7
LENGTH: 246
5229279-7

Query Match 22.0%; Score 287.5; DB 6; Length 246;
Best Local Similarity 31.9%; Pred. No. 8.8e-24;
Matches 81; Conservative 45; Mismatches 109; Indels 19; Gaps 7;

QY 12 VAVITGASGLGATARLYVGOGASAVLLDPPSSGGAGAKKGNKVFAPADVTS 67
DB 5 IAYTGGGIGIGTALICQRLAKDGRVAVAGCGPNSPREKMLEQOKALGFDFIASSEGVAD 64
QY 68 EKDVOITALALAKGFRGVADVAVNAGIIVASKIYNLKKQTHLEDFQRYLDVNLGTFNV 127
DB 65 WDKRTAFDKYSEVGEDVILINNAGI--TRDYVERK--MTRADDAVIDINLSLEFN 118
QY 128 VIRIYAGEMQNEPDGOGGVYIINTASVAAFEQVQAAYSASKGIYGMTPIARDL 187
DB 119 VTKQVIDGMA----DRGW--GRIVNISVNGKQCFQTVNSTRKAGLHGFTALAQEVA 172
QY 188 IGIKMTIAPGLFETPLTSLPEKYNFLASQVFPFSPRLGDPAEVHLYQ--ATTENPFL 246
DB 173 RGIIVNVVAPGFLETDMTRALSDDOAGILAQVP-AGRLGGAQEIANNVAFLASDEAAVI 230
QY 246 NGEVIRLDGAIRM 259
DB 232 STGADFSINGLHM 245

RESULT 17
5512669-4
Patent No. 5512669
APPLICANT: PEOPLES, OLIVER P.; SINSKEY, ANTHONY J.
TITLE OF INVENTION: GENE ENCODING BACTERIAL ACETOACETYL-COA
REDUCTASE
NUMBER OF SEQUENCES: 7
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,667
FILING DATE: 29-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 124,570
FILING DATE: 20-SEP-1993
APPLICATION NUMBER: 944,488
FILING DATE: 03-NOV-1992
APPLICATION NUMBER: 566,535

Thu Jun, 26 06:55:04 2003

us-09-931-186-20.ra1

Page 9

;; FILING DATE: 13-AUG-1990
;; APPLICATION NUMBER: 67,695
;; FILING DATE: 29-JUN-1987
;; SEQ ID NO: 4
;; LENGTH: 273
5512669-4

Query Match 21.7%; Score 282.5; DB 6; Length 273;
Best Local Similarity 31.5%; Pred. No. 3,8e-23;
Matches 90; Conservative 42; Mismatches 91; Indels 63; Gaps 11;

QY 12 VAVITGASGIGLATAEELVGGASAVLLDLPNSGGEAOAKLGNVCAPAF-----63
DB 4 VALVTGSGRGIG-----AAISILKNAAGYKVAAYAGNDAAKPKAENGIAV 51
QY 64 ---DYTESEKDVQFALALAKGKFRVDVAVNCAGIAVAASKTYNKKQGTHTLEDFORVLT 118
DB 52 YKMDVSSYEACVEGIAVEADLPIDLVNNAGIT-----KDMFKMTPDQNNAVI 103
QY 119 DVNLKGTENVI-----RLV-----AGEGQ-NEPDGGQR-----GVIIIN 152
DB 104 NTNLTGLFNTHPYWSGMRDRSFRGIYNTISSINGQKQOMQANYSWSGMRDRSFRGIYV 163
QY 153 TASYAFAFGVGOAAYASASKGIVGMLPIARDLPIGIRVMTIAPGLTGLTSLPEK 212
DB 164 ISSINGQKQOMQANYSAKAGDLGFTKALAGSAGKITVANAICGYITGEMVRAIPK 223
QY 213 VAN-FLASOVPEPSRLDPAEVAHLV--QAIENPLNGEVIPLDG 255
DB 224 VLNERIIPQIPV-GRLEGPDEIARIYVFLASDEAGFTIGSTISANG 268

RESULT 18

US-09-134-001C-4431
Sequence 4431, Application US/09134001C
Patent No. 6380370

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GNC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4431
LENGTH: 274
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4431

Query Match 21.5%; Score 280.5; DB 4; Length 274;
Best Local Similarity 31.7%; Pred. No. 6,3e-23;
Matches 85; Conservative 45; Mismatches 93; Indels 45; Gaps 8;

QY 12 VAVITGASGIGLATAEELVGGASAVLLDLP-----NSGGEAOAKLGNVCAPAF 60
DB 10 IAVITGASTGIGASAVALLAEAGHVLALDISDLEFVOSINDNGSKATAYV-----63
QY 61 APADYSEKDVQFALALAKGKFRVDVAVNCAGIAVAASKTYNKKQGTHTLEDFORVLT 118
DB 64 ---DISDKQYKQSEKIAQEFHVDVFNNAAGVDNA-----GHIHPEYVETDKIN 113
QY 119 DVNLKGTENVIYLAAGMONEPDGGGQGVYINTASVAAFEVGOAATASASKGIVGM 178
DB 114 AVDMGTPLVTKFL-----PLMKRGGSIINTASFGADLVYSSGNAKAGVAIN 166
QY 179 TPIARDLPIGIRVMTIAPGLTGLTSLPEKVAFLASQ-VPEPSRLGDPA 231
DB 167 TKSITAEYGRNIRANATAPGTIEPLVDNLAGTSDEAGQTFENNGKWTPLGRIGTID 226

QY 232 EYAHVVO--AIENPLNGEVIPLDGAI 257
DB 227 EVGRIVAFASDSSSFTETIRIDGIV 254

RESULT 19

US-09-134-001C-4825
Sequence 4825, Application US/09134001C
Patent No. 6380370

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GNC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4825
LENGTH: 249
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4825

Query Match 21.1%; Score 275.5; DB 4; Length 249;
Best Local Similarity 29.1%; Pred. No. 2e-22;
Matches 74; Conservative 54; Mismatches 105; Indels 21; Gaps 6;

QY 13 AVITGASGIGLATAEELVGGASAVLLDLPNSGGEAOA-----KLGNNVCAPADYVS 67
DB 10 ALVTGASGIGRSTALDLAEAGIN-VAVNAGSKDYAEAYEIRAKGVESRILQANYAK 68
QY 68 EKDVQFALALAKGKFRVDVAVNCAGIAVAASKTYNKKQGTHTLEDFORVLDVNLKGTEN 127
DB 69 GDEVKEMIKVEVSGFSDVLYVNNAGITKNDLMPKME-----QEMDVVIDTNKGVEN 122
QY 128 VIRVAGMONEPDGGGQGVYINTASVAAFEVGOAAYASASKGIVGMLPIARDL 187
DB 123 CIQVTPQIMRQ-----KSGALINTSIVGAMNPOQANYATYAGVIGITTAARELA 176
QY 188 PIGIRVMTIAPGLTGLTSLPEKVAFLASOVPEPSRLGDPAEVAHLVQAIEN--PF 245
DB 177 SRGITVNAVADGFIYSDMTNLSDDLKDMLEQIPL-KRGEEDTIDANTVAFASQAKY 235
QY 246 LMGVYIRLDGAI 259
DB 236 ITGQTIHVNGNTM 249

RESULT 20

US-09-238-481-2
Sequence 2, Application US/09238481
Patent No. 6110704

GENERAL INFORMATION:
APPLICANT: Huang, Jiansheng
APPLICANT: McDevitt, Damien
TITLE OF INVENTION: Fabg
FILE REFERENCE: GM10192
CURRENT APPLICATION NUMBER: US/09/238,481
CURRENT FILING DATE: 1999-01-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 246
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-238-481-2

Query Match 20.8%; Score 271.5; DB 3; Length 246;

Best Local Similarity 28.7%; Pred. No. 5.3e-22;
Matches 73; Conservative 57; Mismatches 103; Indels 21; Gaps 6;

QY 13 AVITGASGLGATAEKLVGQASAVLLDLPNSGGEAQA-----KKGNNCFAPADYTS 67
DB 7 ALVTGASRGIGRSIALDLAEEGYN-VAVNYAGSKKEKAEEVEIKAGVSPFALQANVAD 65
QY 68 EKDVOTALALAKGFEGRVAVNACAGIAVASKTYNKKQGTHTLEDFORVLDVNLMTGN 127
DB 66 ADEKAMIKKEYVSQFSLDVLVNNAGITRDLMLRME-----QEMDVIDTNLKGVEN 119
QY 128 VIRLVAGMGQNEPDGQGRVITNTASVAAFEGVQQAAYSASKGIYGMPLPIARDLA 187
DB 120 CIOKATPQMLRO-----RSGAIINTSSVYGAAGNPGQANVATKAGVIGLTFSAARELA 173
QY 188 PIGIRVMTIAPGLGFTPLTSLPEKVFANFLASQVFPFSLDPAEVAHLVQALLEN--PF 245
DB 174 SRGITVNAVAPGFIVSDMTDALSDLEKQMLTQPL-ARFGQDTDIANTVAFSLASDRAXY 232
QY 246 LNGEVIIRLDGAIRM 259
DB 233 ITGQTIHVNGGMYM 246

RESULT 21
US-09-572-810A-2
Sequence 2, Application US/09572810A

Patent No. 6365387
GENERAL INFORMATION:
APPLICANT: Huang, Jianzhong
APPLICANT: McDevitt, Damien
TITLE OF INVENTION: Fabg
FILE REFERENCE: GM10192
CURRENT APPLICATION NUMBER: US/09/572, 810A
CURRENT FILING DATE: 2000-05-17
PRIOR APPLICATION NUMBER: 09/238, 481
PRIOR FILING DATE: 1999-01-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 246
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-572-810A-2

Query Match 20.8%; Score 271.5; DB 4; Length 246;
Best Local Similarity 28.7%; Pred. No. 5.3e-22;
Matches 73; Conservative 57; Mismatches 103; Indels 21; Gaps 6;

QY 13 AVITGASGLGATAEKLVGQASAVLLDLPNSGGEAQA-----KKGNNCFAPADYTS 67
DB 7 ALVTGASRGIGRSIALDLAEEGYN-VAVNYAGSKKEKAEEVEIKAGVSPFALQANVAD 65
QY 68 EKDVOTALALAKGFEGRVAVNACAGIAVASKTYNKKQGTHTLEDFORVLDVNLMTGN 127
DB 66 ADEKAMIKKEYVSQFSLDVLVNNAGITRDLMLRME-----QEMDVIDTNLKGVEN 119
QY 128 VIRLVAGMGQNEPDGQGRVITNTASVAAFEGVQQAAYSASKGIYGMPLPIARDLA 187
DB 120 CIOKATPQMLRO-----RSGAIINTSSVYGAAGNPGQANVATKAGVIGLTFSAARELA 173
QY 188 PIGIRVMTIAPGLGFTPLTSLPEKVFANFLASQVFPFSLDPAEVAHLVQALLEN--PF 245
DB 174 SRGITVNAVAPGFIVSDMTDALSDLEKQMLTQPL-ARFGQDTDIANTVAFSLASDRAXY 232
QY 246 LNGEVIIRLDGAIRM 259
DB 233 ITGQTIHVNGGMYM 246

RESULT 22
US-09-134-001C-4397
Sequence 4397, Application US/09134001C

Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCO
TITLE OF INVENTION: EPIDEMIOIDS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134, 001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064, 964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055, 779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4397
LENGTH: 231
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4397

Query Match 20.6%; Score 269; DB 4; Length 231;
Best Local Similarity 33.3%; Pred. No. 9.1e-22;
Matches 66; Conservative 39; Mismatches 81; Indels 12; Gaps 2;

QY 8 VKGLVAVITGASGLGATAEKLVGQASAVLLDLPNSGGEAQAAGLNNCFAPADYTS 67
DB 5 VKERVAAYVTGASGIGGALANKLSQOGASIVLGRNEQRINLETVOQLNPAKVYADYTV 64
QY 68 EKDVOTALALAKGFEGRVAVNACAGIAVASKTYNKKQGTHTLEDFORVLDVNLMTGN 127
DB 65 KSNIDMLKAVIDHFGHIDLVNSAGSLSKITD-----YVEQMDIMIDVNINGTILH 118
QY 128 VIRLVAGMGQNEPDGQGRVITNTASVAAFEGVQQAAYSASKGIYGMPLPIARDLA 187
DB 119 VLQATLELYLKO-----SSGHIIINTASVGEFPTKNAVYATKAAIHAIQTSLERELA 172
QY 188 PIGIRVMTIAPGLGFTPL 205
DB 173 RTGVKATISBGMKDTDM 190

RESULT 23
US-08-440-856A-3
Sequence 3, Application US/08440856A
Patent No. 5750873

GENERAL INFORMATION:
APPLICANT: DELAPORTA, STEPHEN L. METHODS FOR PRODUCING
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVE. N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440, 856A
FILING DATE: 15-MAY-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 05463-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1517
TELEFAX: (202) 887-0763
TELEX: 706141

; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 337 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ;
 ; US-08-440-856A-3

Query Match 20.6%; Score 268.5; DB 1; Length 337;
 Best Local Similarity 30.9%; Pred. No. 1.9e-21;
 Matches 88; Conservative 44; Mismatches 112; Indels 41; Gaps 6;

QY 6 RSVKGLAVITGASGLTARLVOGASAVLLDLPNSGGEAOKKIGNNCFAPADY 65
 DB 51 KRDKGVAIVTGGARGIGBALVRLFAKHGARRVYADIDDAAGELASALGPQVSFRCDY 110
 QY 66 TSEKDVOTALAKGKF-GRVDYAVNCAGIAVASKTYNLKKGQTHLEDFOQVLDVNLNG 124
 DB 111 SVEEDVRAVDWALSRHGRGLDYCNAGY-LGRQTRARSLSPDAEEDVLRVNALG 169
 QY 125 TENVIRLVAGEMGNEDGGQGVIIINTASVAFEGVQQAAYSASKGIYGMTLPIDAR 184
 DB 170 AALGKHAARAPR-----RGSIVSVASVAVLGGIGPAHYTASKHAIVGLTNAC 223
 QY 185 DLAPIGIRVMTIAPGLFGLPL-----TSLP-----EK 212
 DB 224 ELRHGVRVNCVSPFGVATPMLINAWRQHDATADARDLDLDLVTVPSDQEVEMKE 283
 QY 213 VANFLASQVPPPSRLGDPARYAHVQAIIENPFLNGEVITLDGAI 257
 DB 284 VVRGLATLKGPTLRPRDIAR-AVLFLASDEARYISGHNLVYDGV 327

RESULT 24

; Sequence 270, Application US/08858207A
 ; Patent No. 6348328
 ; GENERAL INFORMATION:
 ; APPLICANT: Black, Michael
 ; APPLICANT: Hodgson, John
 ; APPLICANT: Knowles, David
 ; APPLICANT: Nicholas, Richard
 ; APPLICANT: Stodola, Robert
 ; TITLE OF INVENTION: No. 6348328e1 Compounds
 ; NUMBER OF SEQUENCES: 552
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Smithline Beecham Corporation
 ; STREET: 709 Swedeland Road
 ; CITY: King of Prussia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19406-0939
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/858,207A
 ; FILING DATE: 09-MAY-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/017670
 ; FILING DATE: 14-MAY-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Gimml, Edward R
 ; REGISTRATION NUMBER: 38,891
 ; REFERENCE/DOCKET NUMBER: P50475
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-270-4478
 ; TELEFAX: 610-270-5090
 ;
 ; INFORMATION FOR SEQ ID NO: 270:

; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 186 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: No. 6348328e
 ;
 ; US-08-858-207A-270

Query Match 20.6%; Score 268; DB 4; Length 186;
 Best Local Similarity 38.7%; Pred. No. 8.4e-22;
 Matches 74; Conservative 23; Mismatches 72; Indels 22; Gaps 5;

QY 15 ITGSGAGLATARLVOGASAVLLDLPNSGGE-----AOAKKIGNNCFAPADY 68
 DB 10 ITGSSRGIGLAAHKAFAQAGNIYL-----NSGALSELLAEFSVGIKVPISGVSDF 65
 QY 69 KDVGOTALAKGKFGVDYAVNCAGIAVASKTYNLKKGQTHLEDFOQVLDVNLNGTFNV 128
 DB 66 ADAKRIWDAIAELSGSVLVYNNAGI--TODTIMIKM-----TEADFEKVLKYNLTGAFNM 119
 QY 129 IRLVAGEMGNEDGGQGVIIINTASVAFEGVQQAAYSASKGIYGMTLPIDAR 188
 DB 120 TOSVL-----KPMKARAGALITNMSVYGLMGNIGQANYASKAGLIGFTKSVAREVAS 173
 QY 189 IGRVMTIAPG 199
 DB 174 RNIRRVYIAPG 184

RESULT 25

; Sequence 14, Application US/09504358
 ; Patent No. 6365376
 ; GENERAL INFORMATION:
 ; APPLICANT: Rouviere, Pierre E
 ; APPLICANT: Brzostowicz, Patricia C
 ; TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDI
 ; FILE REFERENCE: BCI001 US NA
 ; CURRENT APPLICATION NUMBER: US/09/504,358
 ; CURRENT FILING DATE: 2000-02-15
 ; EARLIER APPLICATION NUMBER: 60/120,702
 ; EARLIER FILING DATE: 1999-February-19
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 14
 ; LENGTH: 256
 ; TYPE: PRN
 ; ORGANISM: Brevibacterium sp HCU
 ;
 ; US-09-504-358-14

Query Match 20.5%; Score 267; DB 4; Length 256;
 Best Local Similarity 30.9%; Pred. No. 1.8e-21;
 Matches 82; Conservative 39; Mismatches 116; Indels 28; Gaps 8;

QY 10 GLVAVITGASGLTARLVOGASAVLLDLPNSGGEAOKKIGNNCFAPADY 66
 DB 6 GKAIVITGAGAGRIQSELYASEGQVAVVVDNEGSRATDAIRASGVANVYKLDVS 65
 QY 67 SEKDVOOTALAKGKRGVDYAVNCAGIAVASKTYNLKKGQTHLEDFOQVLDVNLNG 124
 DB 66 DESEVEIIVSDAKRGAIVNLYNNAGVGAOK-----PHEIDERLDLVLSVDVG 118
 QY 125 TENVIRLVAGEMGNEDGGQGVIIINTASVAFEGVQQAAYSASKGIYGMTLPIDAR 184
 DB 119 VEFMTKHCIPIFQ-----AGS--GALVNSASIGVSGDELPIYHAKAAYVALTQDAV 172
 QY 185 DLAPIGIRVMTIAPGLFGLPLTSLPEK-----VANFLASQVPPPSRLGDPARY--AH 235
 DB 173 TYGPNIRVAVAPGILPLVYKELSRGPDGIDGXTKLMGAKHPL-GRVGPPEEVAAT 231
 QY 236 LVQAIIENPFLNGEVIRLDGAIRMQ 260
 DB 232 LFLASEBASITIGAVLPVDOGTYAQ 256

Thu Jun 26 06:55:04 2003

us-09-931-186-20.ra1

Page 12

Search completed: June 23, 2003, 14:35:43
Job time : 13.1667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:22:37 ; Search time 31.6667 Seconds
(without alignments)
1698.262 Million cell updates/sec

Title: US-09-931-186-23
Perfect score: 1304
Sequence: 1 MAACRSVKGLAVITGGAS.....ENPFLNGEYIRLDGAIKMP 261

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: SP archaea:
2: SP bacteria:
3: SP fungi:
4: SP human:
5: SP invertebrate:
6: SP mammal:
7: SP mnc:
8: SP organelle:
9: SP phage:
10: SP plant:
11: SP rodent:
12: SP virus:
13: SP vertebrate:
14: SP unclassified:
15: SP viirus:
16: SP bacteriophage:
17: SP archaea:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1240.5	95.1	252	4	Q96hd5 homo sapien
2	1159	88.9	261	11	Q99n15 mus musculu
3	1155	88.6	261	11	Q99n15 mus musculu
4	983	75.4	196	4	Q8rcv9 homo sapien
5	751	57.6	258	5	Q19102 caenorhabdi
6	722	53.4	255	16	Q91070 pseudomonas
7	714	53.4	255	16	Q8rbs0 bruceella me
8	692.5	53.1	252	16	Q8xw0 raietonia s
9	674.5	51.7	250	16	Q06544 mycobacteri
10	673	51.6	255	16	Q92ys1 rhizobium m
11	670	51.4	253	16	Q98hm4 rhizobium 1
12	654	50.2	255	2	Q9ahv1 pseudomonas
13	645	49.7	257	16	Q8ufi2 agrobacteri
14	609	46.7	126	11	Q9dcs5 mus musculu
15	602.5	46.2	264	5	Q8r2l7 dictyosteli
16	598	45.9	260	16	Q9abn6 caulobacter
17	386	29.6	443	2	Q93s33 myxococcus
18	376.5	28.9	246	16	Q8xh11 clostridium
19	358.5	27.5	244	16	Q99yd6 streptococ
20	354	27.1	252	16	Q9hm15 pseudomonas
21	345.5	26.5	249	16	Q97da6 clostridium
22	340.5	26.1	247	16	Q8r9w0 thermococ
23	337.5	25.9	251	16	Q8ryw0 anabaena sp
24	336.5	25.8	246	16	Q9ka03 bacillus ha
25	335.5	25.7	297	3	Q42774 neurospora
26	331	25.4	246	16	Q9k636 bacillus ha
27	329.5	25.3	248	2	Q9krf1 thauera aro
28	328.5	25.2	243	16	Q9fbc3 streptococ
29	327.5	25.1	243	16	Q9chf7 lactococcus
30	325.5	25.0	260	16	Q88068 streptomyce
31	325	24.9	262	2	Q919f8 streptomyce
32	325	24.8	271	10	Q94g09 cucumis sat
33	322.5	24.7	260	4	Q96kr9 homo sapien
34	321	24.6	261	13	Q8t0m4 oryzias lat
35	321	24.6	263	16	Q9kym4 streptomyce
36	320	24.5	271	10	Q94g10 cucumis sat
37	319	24.5	258	2	Q9efv0 streptomyce
38	317.5	24.3	246	2	Q9ex74 macaca mula
39	317.5	24.3	261	6	Q8wmn4 agrobacteri
40	316.5	24.3	259	16	Q80616 sulfolobus
41	316	24.2	299	17	Q97uk6 thauera aro
42	314.5	24.1	249	2	Q9ajr2 streptomyce
43	313.5	24.0	313	2	Q93hc0 xylella fas
44	313	24.0	247	16	Q9epf6 bruceella me
45	313	24.0	262	16	Q8yd94 pyrococcus
46	312.5	24.0	240	17	Q90y54 agrobacter
47	312.5	24.0	296	16	Q9abx6 caulobacter
48	312	23.9	237	4	Q8wtw8 homo sapien
49	311.5	23.9	244	16	Q82f75 yersinia pe
50	310.5	23.8	260	17	Q8u3b3 pyrococcus
51	310	23.8	267	10	P93697 vigna ungu
52	309	23.7	256	16	Q8z8b6 yersinia pe
53	308	23.6	253	16	Q80759 agrobacteri
54	306.5	23.5	247	16	Q80759 listeria mo
55	304.5	23.4	247	16	Q92ak1 listeria in
56	304	23.3	273	2	Q9f5j1 streptomyce
57	303.5	23.3	236	11	Q91vt4 mus musculu
58	303	23.2	247	2	Q92f93 bacillus me
59	302.5	23.2	249	2	Q9lbg5 geobacillus
60	302	23.2	248	16	Q809b5 agrobacteri
61	302	23.2	250	2	Q56840 xanthobacte
62	302	23.2	252	17	Q95s57 streptomyce
63	300	23.0	263	17	Q970a4 sulfolobus
64	299.5	23.0	296	5	Q9xx28 caenorhabdi
65	297.5	22.8	254	16	Q92p88 rhizobium m
66	297.5	22.8	258	16	Q33339 mycobacteri
67	297.5	22.8	538	2	Q8vm75 rhizobium s
68	296	22.7	245	16	Q8r2m1 bruceella me
69	296	22.7	255	17	Q9h041 halobacteri
70	296	22.7	258	16	Q93015 rhizobium m
71	295	22.6	260	16	Q9f8t1 streptomyce
72	295	22.6	315	10	Q949m3 brassica na
73	295	22.6	320	10	Q93x62 brassica na
74	294.5	22.6	267	2	Q9lbg2 leifsonia a
75	294	22.6	265	16	Q9s2e4 streptomyce
76	294	22.5	328	10	Q93x67 brassica na
77	293	22.5	255	16	Q8rdg3 thermococ
78	293	22.5	272	16	Q8rhe0 bruceella me
79	292.5	22.4	405	16	Q98as0 rhizobium 1
80	292	22.4	246	2	Q98as0 streptomyce
81	291.5	22.4	270	4	Q93hm3 homo sapien
82	291.5	22.3	254	10	Q949m2 brassica na
83	290.5	22.3	303	4	Q9bpx1 arabidopsis
84	290.5	22.2	245	16	Q8rdh9 thermococ
85	289.5	22.1	244	16	Q8x815 escherichia
86	288.5	22.1	254	16	Q9rt26 delnocooccus
87	287.5	22.0	256	17	Q8rt15 methanococ
88	287	22.0	243	16	Q8rg25 fusobacteri

90 287 22.0 252 16 092pp0 092pp0 rhizobium m
 91 286.5 22.0 246 2 09pf59 09pf59 streptomyc
 92 286.5 22.0 247 2 0930p0 0930p0 azotobacter
 93 286 21.9 275 16 09k4h0 09k4h0 streptomyc
 94 286 21.9 317 10 093x68 093x68 brassica na
 95 285.5 21.9 246 2 09R880 09R880 burholderi
 96 285.5 21.9 257 16 09WYD3 09WYD3 thermotoga
 97 285.5 21.9 272 16 099RG1 099RG1 staphylococ
 98 285 21.8 255 16 09PC02 09PC02 xyliella fas
 99 284.5 21.8 253 2 09CH41 09CH41 lactococcus
 100 283.5 21.7 248 2 08V0F2 08V0F2 azoarcus ev

ALIGNMENTS

RESULT 1
 096HDS PRELIMINARY; PRT; 252 AA.
 ID 096HDS
 AC 096HDS;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Similar to hydroxyacyl-coenzyme A dehydrogenase, type II.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RL Strausberg R;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC EMBL: BC008708; AA08708.1; -.
 CC InterPro: IPR002198; ADH_short.
 CC Pfam: PF00106; adh_short; 1.
 CC PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.
 KM Oxidoreductase.
 SQ SEQUENCE 252 AA; 25984 MW; F36B71070CE872D CRC64;

Query Match 95.1%; Score 1240.5; DB 4; Length 252;
 Best Local Similarity 96.2%; Pred. No. 4.4e-78;
 Matches 251; Conservative 0; Mismatches 1; Indels 9; Gaps 1;

QY 1 MAAACRSYKGLVAVITGGASGLGATAEELVGGASAVLLDLPNSGGEAQAQKLGNNCF 60
 DB 1 MAAACRSYKGLVAVITGGASGLGATAEELVGGASAVLLDLPNSGGEAQAQKLGNNCF 60
 QY 61 APADVTSEKDVQATLALAKGKFGKRDVAVNCAAGIAVASKTYNLRKGGTHLEDFQRLDV 120
 DB 61 APADVTSEKDVQATLALAKGKFGKRDVAVNCAAGIAVASKTYNLRKGGTHLEDFQRLDV 120
 QY 121 NLMTGFNVIRLVAGEMGNEPDGGGGRVITNTASVAFAEGVGQAAYSASKGIVGNTL 180
 DB 121 NLMTGFNVIRLVAGEMGNEPDGGGGRVITNTASVAFAEGVGQAAYSASKGIVGNTL 180
 QY 121 NLMTGFNVIRLVAGEMGNEPDGGGGRVITNTASVAFAEGVGQAAYSASKGIVGNTL 180
 DB 121 NLMTGFNVIRLVAGEMGNEPDGGGGRVITNTASVAFAEGVGQAAYSASKGIVGNTL 180
 QY 181 PIARDLAPGIRVMTIAPGLFGPPLTSLPEKVSNTLASQVFPSPRLGDPAYAHLYQAI 240
 DB 181 PIARDLAPGIRVMTIAPGLFGPPLTSLPEKVSNTLASQVFPSPRLGDPAYAHLYQAI 240
 QY 181 PIARDLAPGIRVMTIAPGLFGPPLTSLPEKVSNTLASQVFPSPRLGDPAYAHLYQAI 240
 DB 181 PIARDLAPGIRVMTIAPGLFGPPLTSLPEKVSNTLASQVFPSPRLGDPAYAHLYQAI 240
 QY 241 IENPFLNGEYIRLDGAIRMOP 261
 DB 241 IENPFLNGEYIRLDGAIRMOP 261
 QY 232 IENPFLNGEYIRLDGAIRMOP 252
 DB 232 IENPFLNGEYIRLDGAIRMOP 252

RESULT 2
 099N15 PRELIMINARY; PRT; 261 AA.
 ID 099N15
 AC 099N15;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)

DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Short chain L-3-hydroxyacyl-CoA dehydrogenase.
 GN HSD17B10 OR SCHAD.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21095701; PubMed=1165016;
 RA He X.Y., Kertz G., Chu C.H., Lin D., Yang Y.Z., Menta P., Schulz H.,
 RA Yang S.Y.;
 RA "Molecular cloning, modeling, and localization of rat type 10 17beta-
 RT hydroxysteroid dehydrogenase.";
 RL Mol. Cell. Endocrinol. 171:89-98(2001).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC EMBL: AF233685; AKI15008.1; -.
 CC HSSP: O70351; 1E6W.
 CC MGD: MGI:133871; Hsd17b10.
 CC InterPro: IPR002198; ADH_short.
 CC Pfam: PF00106; adh_short; 1.
 CC PRINTS: PR00080; SDRFAMILY.
 CC PROSITE: PS00061; ADH_SHORT; 1.
 KM Oxidoreductase.
 SQ SEQUENCE 261 AA; 27273 MW; F371ED8A15FCFAF CRC64;

Query Match 88.9%; Score 1159; DB 11; Length 261;
 Best Local Similarity 87.7%; Pred. No. 1.9e-72;
 Matches 229; Conservative 18; Mismatches 14; Indels 0; Gaps 0;

QY 1 MAAACRSYKGLVAVITGGASGLGATAEELVGGASAVLLDLPNSGGEAQAQKLGNNCF 60
 DB 1 MAAACRSYKGLVAVITGGASGLGATAEELVGGASAVLLDLPNSGGEAQAQKLGNNCF 60
 QY 61 APADVTSEKDVQATLALAKGKFGKRDVAVNCAAGIAVASKTYNLRKGGTHLEDFQRLDV 120
 DB 61 APADVTSEKDVQATLALAKGKFGKRDVAVNCAAGIAVASKTYNLRKGGTHLEDFQRLDV 120
 QY 121 NLMTGFNVIRLVAGEMGNEPDGGGGRVITNTASVAFAEGVGQAAYSASKGIVGNTL 180
 DB 121 NLMTGFNVIRLVAGEMGNEPDGGGGRVITNTASVAFAEGVGQAAYSASKGIVGNTL 180
 QY 181 PIARDLAPGIRVMTIAPGLFGPPLTSLPEKVSNTLASQVFPSPRLGDPAYAHLYQAI 240
 DB 181 PIARDLAPGIRVMTIAPGLFGPPLTSLPEKVSNTLASQVFPSPRLGDPAYAHLYQAI 240
 QY 241 IENPFLNGEYIRLDGAIRMOP 261
 DB 241 IENPFLNGEYIRLDGAIRMOP 261

RESULT 3
 09CCT3 PRELIMINARY; PRT; 261 AA.
 ID 09CCT3
 AC 09CCT3;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Hydroxyacyl-coenzyme A dehydrogenase, type II.
 GN HSD17B10 OR HADH2
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arikawa T., Hara A., Fukunishi Y., Kondo H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka T.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kariya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauts P.,
 RA Nodone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 CL Nature 409:685-690(2001),
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 DR EMBL: AK013440; BAB28800.1; -
 DR HSSP: 070351; 1E6W.
 DR MGD: MGI:1333871; Hsd17b10.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.
 DR PRINTS: PRO0080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Oxidoreductase.
 SQ SEQUENCE 261 AA; 27273 MW; F36CD179C7FCEFAF CRC64;

Query Match 88.6%; Score 1155; DB 11; Length 261;
 Best Local Similarity 87.4%; Pred. No. 3.6e-72;
 Matches 228; Conservative 19; Mismatches 14; Indels 0; Gaps 0;
 QY 1 MAACRSYKGLAVITGASGLATAEERLVGASAVLLDLPNSGGEAQAARKLNQCVF 60
 DB 1 MAAYASVKGVLAVVVGASGLGATKRLVGAGATVLLDVPDSGEAQAARKLGSCIF 60
 QY AAPADVTSEKDVQFALALAKGKFRGVAVNACAGIAVASKTYNLKKGQTHLDFORVLDV 120
 DB 61 AAPAVTSEKIDQALALAKGKFRGVAVNACAGIAVASKTYNLKKGQTHLDFORVLDV 120
 QY 121 NLMTGPNVIRLVAGENGQNEPDGGQGVINTASVAEFGQGAAYASAKGIVGML 180
 DB 121 NLIGTFNVIRLVAGENGQNEPDGGQGVINTASVAEFGQGAAYASAKGIVGML 180
 QY 181 PIARDLAPGIRVMTIAPGLFGFPLTSLPEKYSNLAQVPPPSLGPAPYAHLYQAI 240
 DB 181 PIARDLAPGIRVMTIAPGLFGFPLTSLPEKYSNLAQVPPPSLGPAPYAHLYQAI 240
 QY 241 IENPFLNGEYIRLDGAIKMP 261
 DB 241 IENPFLNGEYIRLDGAIKMP 261

RESULT 4
 Q8TCV9 PRELIMINARY; PRT; 196 AA.
 ID 08TCV9
 AC 08TCV9;
 DT 01-JUN-2002 (TEMBLrel. 21, Created)
 DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
 DE Endoplasmic reticulum-associated amyloid beta peptide-binding protein
 DE (Fragment).
 GN ERAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Deininger M.H., Meyermann R., Schluesener H.J.,
 RT "Expression, release and induction of endoplasmic reticulum-associated
 RT amyloid beta-binding protein in brain disease."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY092415; AAM18189.1; -
 FT NON-TER 1
 FT NON-TER 196
 SQ SEQUENCE 196 AA; 20581 MW; 240DE149668AAGA CRC64;
 Query Match 75.4%; Score 983; DB 4; Length 196;
 Best Local Similarity 99.5%; Pred. No. 1.8e-60;
 Matches 195; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 51 AKKIGNNCFAPADVTSEKDVQFALALAKGKFGVAVNACAGIAVASKTYNLKKGQTH 110
 DB 1 AKKIGNNCFAPADVTSEKDVQFALALAKGKFGVAVNACAGIAVASKTYNLKKGQTH 60
 QY 111 LEDFORVLDVNLMTGPNVIRLVAGENGQNEPDGGQGVINTASVAEFGQGAAYSA 170
 DB 61 LEDFORVLDVNLMTGPNVIRLVAGENGQNEPDGGQGVINTASVAEFGQGAAYSA 120
 QY 171 SKGIVGNTPIARDLAPGIRVMTIAPGLFGFPLTSLPEKYSNLAQVPPPSRLGDP 230
 DB 121 SKGIVGNTPIARDLAPGIRVMTIAPGLFGFPLTSLPEKYSNLAQVPPPSRLGDP 180
 QY 231 AEVAHLVQAITEENPFL 246
 DB 181 AEVAHLVQAITEENPFL 196

RESULT 5
 Q19102 PRELIMINARY; PRT; 258 AA.
 ID 019102
 AC 019102;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
 DE Probable 3-hydroxacyl-coA dehydrogenase F01G4.2 type II (EC 1.1.1.35)
 DE (Type II HADH).
 GN F01G4.2.
 GN Caenorhabditis elegans.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditidae;
 OC Rhabditidae; Rhabditidae; Caenorhabditis.
 OX NCBI_TaxID=6259;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Harris B.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: L-3-HYDROXYACYL-COA + NAD(+) = 3-OXOACYL-COA +
 CC NADH.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC FAMILY (SDR).
 CC EMBL: Z68341; CAA92764.1; -
 CC HSSP: 070351; 1E6W.
 DR WormPep: F01G4.2; CE03127.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PRO0080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Hypothetical protein; Oxidoreductase; NAD; Mitochondrion.
 FT NP_BIND 11 36
 FT ACT_SITE 155 165
 FT SEQUENCE 258 AA; 27143 MW; 86BF2568EE6902B3 CRC64;
 Query Match 57.6%; Score 751; DB 5; Length 258;
 Best Local Similarity 59.9%; Pred. No. 2.5e-44;
 Matches 154; Conservative 34; Mismatches 67; Indels 2; Gaps 1;
 QY 3 AACRSYKGLAVITGASGLATAEERLVGASAVLLDLPNSGGEAQAARKLNQCVAP 62
 DB 2 SALRSTKGLVAVVVGASGLGAAEVLAKAGQVAIIDLPQSKADVAKEIGG--ITP 59
 QY 63 ADVTSEKDVQFALALAKGKFGVAVNACAGIAVASKTYNLKKGQTHLDFORVLDVNL 122
 DB 60 ASVTSEBEVRAFAKVAQAEYGRDLAVNACAGIAVAFKLYSYQKKKHVDFEIRIQTIIDVNV 119

QY	123	MGFENVIRLVAEKGQNEPDGGRGVYINTASVAEFGQVGAQSAKSGKQIGMTLPI	182
Db	120	LGFTFNVRHGVALLMGEHKKDANGRGVYINTASVAADGGQGSASKSKALYGMTLPL	179
QY	183	ARDLAPGIRVMTIAPGLFGTLPILTSLEPKVSNFLASOVPPPSRLGDPAEYAHVQAITE	242
Db	180	ARFAGAGGIRNMTIAPGLMDPILTSLEPKVSYLAQLIPNPSRLGHPHEYGALVQHITE	239
QY	243	NPELNGEVIRLDGAIRM	259
Db	240	NOYLNGETIRPDGALRM	256
RESULT 6			
Q910T0 PRELIMINARY; PRT: 255 AA.			
AC	Q910T0		
DT	01-MAR-2001 (TREMBlrel. 16, Created)		
DT	01-MAR-2001 (TREMBlrel. 16, last sequence update)		
DT	01-MAR-2002 (TREMBlrel. 20, last annotation update)		
DE	Probable short-chain dehydrogenase.		
GN	PA2554.		
OS	Pseudomonas aeruginosa.		
OC	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;		
OC	Pseudomonas.		
OX	NCBI_Taxid=287;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-ATCC 15692 / PA01;		
RX	MEDLINE=20437337; PubMed=10984043;		
RA	Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,		
RA	Hickey M.J., Birkman F.S.L., Hutnagle W.O., Kowalik D.J., Lagrou P.,		
RA	Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,		
RA	Brody L.L., Coulter S.N., Tolinger K.R., Kas A., Lazdiz K., Lam R.M.,		
RA	Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,		
RA	Reizer J., Salier M.H., Hancock R.E.W., Iori S., Olson M.V.,		
RT	"Complete genome sequence of Pseudomonas aeruginosa PA01, an		
RT	opportunistic pathogen."		
RL	Nature 406:959-964(2000)."		
CC	-1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES		
CC	(SDR) FAMILY.		
DR	HMBL; AE004683; AAC05942.1; -.		
DR	HSSP; O70351.1E3S.		
DR	InterPro: IPR002198; ADH_short.		
DR	Pfam: PF00106; adh_short.1.		
DR	PRINTS; PR00080; SDRFAMILY.		
DR	PROSITE; PS00061; ADH_SHORT; 1.		
KW	Oxidoreductase; Complete proteome.		
SO	SEQUENCE 255 AA; 26426 MW; EB8FF28712D2936D CRC64;		
Query Match 55.4%; Score 722; DB 16; Length 255;			
Best Local Similarity 57.5%; Pred. No.2.5e-42;			
Matches 145; Conservative 35; Mismatches 66; Indels 2; Gaps 1;			
QY	8	VKGLVYITGASGLGATAERLVGGASAVLLDIPNSGEPDAKKTGNCVFAPADYTS	67
Db	3	IENRFVLTVGGSSGGATATKMLVEQGGKVVLAIDINARAGAKAEELGAQARFADATAS	62
QY	68	EKDVTALALAKKGFGRVADVAVNAGIYVASKTYNLKKGTHTLEDFQRYLDVNMGTFN	127
Db	63	EADGRQAVAAALAEAFGGHGLNLCAGVAPARKV--LGRNGIHALESFRRVINDINVGSEFN	120
QY	128	VIRLVAGMGNEPDGGQGRVYINTASVAEFGQVGAQSAKSGKQIGMTLPIARDLA	187
Db	121	MLRLAAEEMSGOGDPDEGGERVYINTASVAADFQIGGAAASAKSGVAGMTLPIARELA	180
QY	188	PIGIRVMTIAPGLFGTLPILTSLEPKVSNFLASOVPPPSRLGDPAEYAHVQAITE	247
Db	181	RFGIRVMTIAPGIFETPRMAQMPCEVRVDSLGASVDFPRLGRDPDYALVRQIENSMKN	240
QY	248	GEVIRLDGAIRM	259
Db	241	GEVIRLDGAIRM	252

Query	Subject	Score	Length	Ident
Q1	Q1	54.8%	714	100%
Q2	Q2	57.1%	884	95%
Q3	Q3	37.1%	69	2%
Q4	Q4	69.1%	120	100%
Q5	Q5	69.1%	120	100%
Q6	Q6	69.1%	120	100%
Q7	Q7	69.1%	120	100%
Q8	Q8	69.1%	120	100%
Q9	Q9	69.1%	120	100%
Q10	Q10	69.1%	120	100%
Q11	Q11	69.1%	120	100%
Q12	Q12	69.1%	120	100%
Q13	Q13	69.1%	120	100%
Q14	Q14	69.1%	120	100%
Q15	Q15	69.1%	120	100%
Q16	Q16	69.1%	120	100%
Q17	Q17	69.1%	120	100%
Q18	Q18	69.1%	120	100%
Q19	Q19	69.1%	120	100%
Q20	Q20	69.1%	120	100%
Q21	Q21	69.1%	120	100%
Q22	Q22	69.1%	120	100%
Q23	Q23	69.1%	120	100%
Q24	Q24	69.1%	120	100%
Q25	Q25	69.1%	120	100%
Q26	Q26	69.1%	120	100%
Q27	Q27	69.1%	120	100%
Q28	Q28	69.1%	120	100%
Q29	Q29	69.1%	120	100%
Q30	Q30	69.1%	120	100%
Q31	Q31	69.1%	120	100%
Q32	Q32	69.1%	120	100%
Q33	Q33	69.1%	120	100%
Q34	Q34	69.1%	120	100%
Q35	Q35	69.1%	120	100%
Q36	Q36	69.1%	120	100%
Q37	Q37	69.1%	120	100%
Q38	Q38	69.1%	120	100%
Q39	Q39	69.1%	120	100%
Q40	Q40	69.1%	120	100%
Q41	Q41	69.1%	120	100%
Q42	Q42	69.1%	120	100%
Q43	Q43	69.1%	120	100%
Q44	Q44	69.1%	120	100%
Q45	Q45	69.1%	120	100%
Q46	Q46	69.1%	120	100%
Q47	Q47	69.1%	120	100%
Q48	Q48	69.1%	120	100%
Q49	Q49	69.1%	120	100%
Q50	Q50	69.1%	120	100%
Q51	Q51	69.1%	120	100%
Q52	Q52	69.1%	120	100%
Q53	Q53	69.1%	120	100%
Q54	Q54	69.1%	120	100%
Q55	Q55	69.1%	120	100%
Q56	Q56	69.1%	120	100%
Q57	Q57	69.1%	120	100%
Q58	Q58	69.1%	120	100%
Q59	Q59	69.1%	120	100%
Q60	Q60	69.1%	120	100%
Q61	Q61	69.1%	120	100%
Q62	Q62	69.1%	120	100%
Q63	Q63	69.1%	120	100%
Q64	Q64	69.1%	120	100%
Q65	Q65	69.1%	120	100%
Q66	Q66	69.1%	120	100%
Q67	Q67	69.1%	120	100%
Q68	Q68	69.1%	120	100%
Q69	Q69	69.1%	120	100%
Q70	Q70	69.1%	120	100%
Q71	Q71	69.1%	120	100%
Q72	Q72	69.1%	120	100%
Q73	Q73	69.1%	120	100%
Q74	Q74	69.1%	120	100%
Q75	Q75	69.1%	120	100%
Q76	Q76	69.1%	120	100%
Q77	Q77	69.1%	120	100%
Q78	Q78	69.1%	120	100%
Q79	Q79	69.1%	120	100%
Q80	Q80	69.1%	120	100%
Q81	Q81	69.1%	120	100%
Q82	Q82	69.1%	120	100%
Q83	Q83	69.1%	120	100%
Q84	Q84	69.1%	120	100%
Q85	Q85	69.1%	120	100%
Q86	Q86	69.1%	120	100%
Q87	Q87	69.		

RT Sinorhizobium meliloti pSymA megaplasmid.
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
 DR EMBL: AE007266; AAK65450.1; -
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.
 KW Plasmid: Complete proteome.
 SQ SEQUENCE 255 AA; ED6C7942D3ED867C CRC64;

Query Match 51.6%; Score 673; DB 16; Length 255;
 Best Local Similarity 54.7%; Pred. No. 5.9e-39;
 Matches 139; Conservative 34; Mismatches 79; Indels 2; Gaps 1;

QY 8 VKLVAVITGASGLIATAEERLVGGASAVLLDPSNGGEAOKLGNCCFAPADYTS 67
 DB 3 LKSRFVITGASGLIATAEERLVGGASAVLLDPSNGGEAOKLGNCCFAPADYTS 62
 QY 68 EKDVOITALAKRFRVDVAVNCAGIAVASKTYNKKQOTHTLEDFQVLDVNI MGTFN 127
 DB 63 EADATALAPAKQEFHGVHGLVNCAGTAPGEKI--LGRSGPHALDSFARTVAVNLIGTFN 120
 QY 128 VIRLVAGEMQNPDDGCGRGVITNTASVAAREGGVGAAYASAKSGIYGMTLP IARDIA 187
 DB 121 MIRLAAYVMSQGGEDDGERGVITNTASIAAFDGOIQAAYASAKSGVAAITLP IAREIA 180
 QY 188 PIGIRVWTIAPGLFETPLTSLPEKVSNFLASQVPPPSRLGDAEYAHVQAL IENPFIN 247
 DB 181 REGIRVWTIAPGLFETPLTSLPEKVSNFLASQVPPPSRLGDAEYAHVQAL IENPFIN 240
 QY 248 GEVRLDGAIRMPQ 261
 DB 241 GEVRLDGAIRMAP 254

RESULT 11

Q98HM4 PRELIMINARY; PRT; 253 AA.
 AC Q98HM4
 DT 01-OCT-2001 (TRIMBLrel. 15, Created)
 DT 01-OCT-2001 (TRIMBLrel. 18, Last sequence update)
 DT 01-JUN-2002 (TRIMBLrel. 21, Last annotation update)
 DE 3-hydroxycy1-COA dehydrogenase type II.
 GN MLR2803.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kato T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpoto S.,
 RA Takeuchi C., Yamada M., Tabata S.,
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti".
 RL DNA Res. 7:331-338(2000).
 DR EMBL: AP003000; BAB49842.1; -
 DR InterPro: IPR002198; ADH_short.
 DR InterPro: IPR001092; HLH_basic.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PRO0080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 253 AA; 25814 MW; 8832D90EB9BD32A CRC64;

Query Match 51.4%; Score 670; DB 16; Length 253;
 Best Local Similarity 54.4%; Pred. No. 9.4e-39;
 Matches 137; Conservative 37; Mismatches 74; Indels 4; Gaps 2;

QY 10 GLVAVITGASGLIATAEERLVGGASAVLLDPSNGGEAOKLGNCCFAPADYTSK 69
 DB 5 GQIAIVTGGSGGLBARDRALAAKARVATDVIEAARAAVADIG--ISVCDVSSAD 62
 QY 70 DVOTALAKRFRVDVAVNCAGIAVASKTYNKKQOTHTLEDFQVLDVNI MGTFN 129
 DB 63 SGTALAPATASKLGPRLVNCAGIATGVKT--IGKDGPHLDQYRRVIEVNLIGTFN 120
 QY 130 RLVAGEMQNPDDGCGRGVITNTASVAAREGGVGAAYASAKSGIYGMTLP IARDIA 189
 DB 121 RLVADRAASLEPLDGGEGGVITNTASVAADGLOGAAYASAKSGVGMILP IARDIARS 180
 QY 190 GIRVWTIAPGLFETPLTSLPEKVSNFLASQVPPPSRLGDAEYAHVQAL IENPFIN 249
 DB 181 GIRVCTIAPGLFETPLTSLPEKVSNFLASQVPPPSRLGDAEYAHVQAL IENPFIN 240
 QY 250 VIRLDGAIRMPQ 261
 DB 241 TIRLDGAIRMAP 252

RESULT 12

Q98HY1 PRELIMINARY; PRT; 255 AA.
 AC Q98HY1
 DT 01-JUN-2001 (TRIMBLrel. 17, Created)
 DT 01-JUN-2001 (TRIMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TRIMBLrel. 21, Last annotation update)
 DE FadB2X.
 GN FadB2X.
 OS Pseudomonas putida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-U;
 RX MEDLINE=21150437; PubMed=11251808;
 RA Oliveira E.R., Carricero D., Garcia B., Minambres B., Moreno M.A.,
 RA Canejo L., Dirusso C.C., Naharro G., Luengo J.M.;
 RT "Two different pathways are involved in the b-oxidation of n-alkanoic
 RT and n-phenylalkanoic acids in pseudomonas putida U: genetic studies
 RT and biotechnological applications.";
 RL Mol. Microbiol. 39:863-874(2001).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDS) FAMILY
 DR EMBL: AF290950; AAK18170.1; -
 DR HSSP: O70351; IE3S.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PRO0080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.
 KW Oxidoreductase.
 SQ SEQUENCE 255 AA; 26003 MW; 56B65802E906F73F CRC64;

Query Match 50.2%; Score 654; DB 2; Length 255;
 Best Local Similarity 54.5%; Pred. No. 1.2e-37;
 Matches 134; Conservative 40; Mismatches 70; Indels 2; Gaps 1;

QY 14 VIRGASGLIATAEERLVGGASAVLLDPSNGGEAOKLGNCCFAPADYTSKDYOT 73
 DB 9 IVSGAASGLIATAEERLVGGASAVLLDPSNGGEAOKLGNCCFAPADYTSKDYOT 68
 QY 74 ALALAKRFRVDVAVNCAGIAVASKTYNKKQOTHTLEDFQVLDVNI MGTFN 133
 DB 69 AYDAVAASARGSLQGLVNCAGIYAEV--LGKQGPGLISFAKVIYVNLVGSFNLRLAA 126
 QY 134 GEGVQNPDDGCGRGVITNTASVAAREGGVGAAYASAKSGIYGMTLP IARDIAP IGRV 193
 DB 127 AMAEGADDEAGRGVITNTASVAADGLOGAAYASAKSGIYGMTLP IARDIAP IGRV 186
 QY 194 MTAPGLFETPLTSLPEKVSNFLASQVPPPSRLGDAEYAHVQAL IENPFIN 253
 DB 194 MTAPGLFETPLTSLPEKVSNFLASQVPPPSRLGDAEYAHVQAL IENPFIN 253

Db 187 MTAPGIFETPPMAGTEEVNARSLAGVPPPPRLGRPOEYTAALARIHNSMLNGEVIRL 246
 QY 254 DGAIRM 259
 Db 247 DGAIRM 252

RESULT 13

Q8UF12 PRELIMINARY; PRT; 257 AA.
 AC Q8UF12;
 DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, last annotation update)
 DE 3-hydroxyacyl-CoA dehydrogenase type II.
 GN AT01415 OR AGR_C_2613.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608550; PubMed=11743193;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Okura Y.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boye D. Sr.,
 RA Chapman P., Glendening J., Deatherage G., Gillet W., Grant C.,
 RA Kutayman T., Levy R., Li M.-J., McClelland E., Palmieri A.,
 RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chunley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Nester E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 C58.";
 RL Science 294:2317-2323(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Gurillo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Hounell K., Gordon J., Vaudin D., Scott C., Iapras C., Markelz B.,
 RA Woliam C., Allinger M., Doughty D., Scott C., Iapras C., Markelz B.,
 RA Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
 RA Cleto C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 Agrobacterium tumefaciens C58.";
 RL Science 294:2323-2328(2001).
 DR EMBL: AE009102; AAI42421.1;
 DR EMBL: AE008067; AAK87207.1;
 KW Complete proteome.
 SQ SEQUENCE 257 AA; 26622 MW; FF74A61FFC4B2B5C CRC64;

Query Match 49.5%; Score 645; DB 16; Length 257;
 Best Local Similarity 51.7%; Pred. No. 5e-37;
 Matches 134; Conservative 41; Mismatches 76; Indels 8; Gaps 3;

QY 7 SYKGLVAVITGGASGLGATARLVGGASAVLLDLPSSGGEAQAQKKGNNCYAPADVT 66
 Db 2 NIEGAGALVTGASGLGAIVARMLAARGAAVTIFDRNGEAKKLAELGGRAV--QGVT 59
 QY 67 SEKDVOTALAKGKFGVAVNCAIVASAKTYNKKQTHLTLEFORVLDVNLMTF 126
 Db 60 SDADQQAIAKVAASAKGRLITVNCAGITAGRI--LGRBPPLGDEQYIRNLTSTF 117
 QY 127 NVIRLVAGEKGNEDDQ---GQRGVINTASVAAPFGVGOAASAKSGIYGMPLPI 182
 Db 118 NMMRLAAAHMEREDDEGDSRDQDGVIVNTASVAAPFGVGOAASAKSGIYSLAPA 177
 QY 183 AADLAPIGIRVITAPGLFTPLTSLPEKVSNFLASOVPPSPRGDAEVAHLVOALIE 242
 Db 178 ARELARIRIVNTAVAGIFLPLPLGLPQVQESLAGIIPHSRGLDPAEFAADYVRLIE 237

QY 243 NPELNGEVIRLDGAIRMOP 261
 Db 238 NDYMNGEVIRLDGAIRMOP 256

RESULT 14

Q9DCX5 PRELIMINARY; PRT; 126 AA.
 AC Q9DCX5;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, last annotation update)
 DE Hydroxyacyl-coenzyme A dehydrogenase, type II.
 GN HSD17B10 OR HADH2.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6J; TISSUE=KIDNEY;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai T., Shingawa A., Shidata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Rietschman W., Gaasterland T., Glasl C., King B., Kochiwa H.,
 RA Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shidata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
 RA Wyshaw-Solis A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 (SDR) FAMILY.
 CC EMBL: AK002368; BAB22046.1; -;
 DR HSSP: O70351; 1E6W.
 DR MGD: MGI:1333871; Hsd17b10.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Oxidoreductase.
 SQ SEQUENCE 126 AA; 13265 MW; 78FEB6D41B9989D CRC64;

Query Match 46.7%; Score 609; DB 11; Length 126;
 Best Local Similarity 95.2%; Pred. No. 6.5e-35;
 Matches 120; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 136 MGONEDPQGGORGVYINTASVAAPFEGVGOAASAKSGIGVGTLPARDLAPIGIRVMT 195
 Db 1 MGONEDPQGGORGVYINTASVAAPFEGVGOAASAKSGIGVGTLPARDLAPIGIRVMT 60
 QY 196 IAPLFTPLTSLPEKVSNFLASOVPPSPRGDAEVAHLVOALIEPNPLNGEVIRLDG 255
 Db 61 IAPLFTPLTSLPEKVSNFLASOVPPSPRGDAEVAHLVOALIEPNPLNGEVIRLDG 120
 QY 256 AIRMOP 261
 Db 121 AIRMOP 126
 RESULT 15
 Q8T2L7

Db 8 AVITGXXXRXAGRGPARRPRL---ARSALFDLNDKGAANAVALGADKARFENNVS 63
 Qy 67 SEKDVOFATALAKGKFGKRVAVNCAGIAVASKTYNLKKQGTHTLEDFORVLDVLMKTE 126
 Db 64 DEAAVTAIDQAHDLGLGINVAMNAGILGAGR--LKEGSMPLAGFGGVNVLVGSF 121
 Qy 127 NVIRLVAGMGONPDQGGQGVIIINTASVAAFESQVQAAVSASKGIVGKTLPIADL 186
 Db 122 NVAKAANRMCNENAGTGERGVIIINTASIAVEGOIAQAAVYASKGIVSMILPMAREL 181
 Qy 187 APGIRVMTIAPGLFTPLLTSLPEKV 213
 Db 182 SFGGIRVNTIAPGVMTIAPVMDMPNAV 208

RESULT 18

Q8XHL1 PRELIMINARY: PRT: 246 AA.

AC 08XHL1
 DT 01-MAR-2002 (TEMBLrel. 20, Created)
 DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
 DE 3-oxoacyl-(acyl-carrier-protein) reductase.
 GN FABG OR CPE1070.
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Clostridiaceae; Clostridium.
 NCBI_TaxID=1502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=13 / TYPE A;
 RX PubMed=11792842;
 RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yanashita A.,
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.,
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic
 RT flesh-eater."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 DR EMBL; AP003189; BAB80776.1;
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRfamily.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Complete proteome.
 SQ SEQUENCE 246 AA; 26267 MW; CD90B8C650ECC817 CRC64;

Query Match 28.9%; Score 376.5; DB 16; Length 246;
 Best Local Similarity 35.8%; Pred. No. 1.5e-18;
 Matches 93; Conservative 47; Mismatches 97; Indels 23; Gaps 7;

Qy 8 VKGLVAVITGASGLGATTAERLVGOGASAVLLDLPNSGGEAQAQKL-----GNKCYFAP 62
 Db 2 LKQKVALVTGTRIGRAIALKLDAGAN-IVINTRNSDEAELEKALIEKGVKVLTK 60
 Qy 63 ADVTSEKDVOFATALAKGKFGKRVAVNCAGIAVASKTYNLKKQGTHTLEDFORVLDVNL 122
 Db 61 CDISNFDKSNIMDKCEVFGKIDILVNNAGITRKDILIMRKE-----EDFNVIDVNL 114
 Qy 123 MGTFFNVLRLVAGMGONPDQGGQGVIIINTASVAAFESQVQAAVSASKGIVGKTLPI 181
 Db 115 KGTFNCAKHSALMLK-----ORFGKIINMTSVGIIAGNAGVNSASAKAVIGLTKS 167
 Qy 182 IARLAPLIGIRVMTIAPGLFTPLLTSLPEKVSNFLASQVFPFSLGDDPAEVAHLVQAI 241
 Db 168 LAKLGRSGITVNAVAAGFINTDMTASLSEKVEKESKNIP-L-KRLGDPEDVAVNLVFLA 226
 Qy 242 ENP--FLNGEYIRLDGAIRM 259
 Db 227 SDAANYITGVINVDGGMV 246

RESULT 19
 Q99YD6 PRELIMINARY: PRT: 244 AA.

AC Q99YD6;
 DT 01-JUN-2001 (TEMBLrel. 17, Created)
 DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
 DE Putative beta-ketoacyl-ACP reductase (PC 1.1.1.100).
 GN FABG OR SPY1749.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 NCBI_TaxID=13147;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SF370 / SEROTYPE M1;
 RX MEDLINE=21192684; PubMed=11296296;
 RA Ferretti J.J., Moshan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
 RA Primeaux C., Sezate S., Stvorov A.N., Kenton S., Lai H.S., Lin S.P.,
 RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.,
 RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY
 DR EMBL; AE006603; AAK34493.1; -
 DR HSSE; P50162; IAB1.
 DR InterPro: IPR002198; ADH_short.
 DR InterPro: IPR001092; HLH_basic.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR01608; BACTINVASINC.
 DR PRINTS: PR00080; SDRfamily.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
 KW Oxidoreductase; Complete proteome.
 SQ SEQUENCE 244 AA; 26002 MW; 67ECE23870D40D65 CRC64;

Query Match 27.5%; Score 358.5; DB 16; Length 244;
 Best Local Similarity 35.4%; Pred. No. 2.7e-17;
 Matches 92; Conservative 41; Mismatches 102; Indels 25; Gaps 5;

Qy 8 VKGLVAVITGASGLGATTAERLVGOGASAVLLDLPNSGGEAQAQKL-----GNKCYF 60
 Db 3 IKGNIFITGSTRIGILAMAHQFASLEIANIVL-----NGRAISEELVASPTDYGVTVT 57
 Qy 61 APADVTSEKDVOFATALAKGKFGKRVAVNCAGIAVASKTYNLKKQGTHTLEDFORVLDV 120
 Db 58 ISGDVSEASEAKRVNNEALIESIGSIDVLYNNAGIT-----NDKILMKTEDEDFERYLKI 111
 Qy 121 NMGTFFNVLRLVAGMGONPDQGGQGVIIINTASVAAFESQVQAAVSASKGIVGKTL 180
 Db 112 NLTGAFNNMGQVLT-----KPMIKAROGAIINVSIVGLTGIGICQANAAKAGWIGFTK 165
 Qy 181 PIARLAPLIGIRVMTIAPGLFTPLLTSLPEKVSNFLASQVFPFSLGDDPAEVAHLVQAI 240
 Db 166 SVAREVAARNICVNAIAPGFIESDMGVLPKMQSIIISQIPM-KRIGKAEVAHLASFL 224
 Qy 241 IENPFLNGEYIRLDGAIRM 260
 Db 225 VEDDYITGVINVDGGMVQ 244

RESULT 20

Q9HW15 PRELIMINARY: PRT: 252 AA.

AC Q9HW15
 DT 01-MAR-2001 (TEMBLrel. 16, Created)
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
 DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
 DE Probable short-chain dehydrogenase.
 GN PA4389.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subphylum; Pseudomonadaceae;
 OC Pseudomonas.
 NCBI_TaxID=287;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 15692 / PA01:
 RX MEDLINE-20437337; PubMed-10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Gardner R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Felder K.R., Kas A., Lardig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.,
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PA01, an
 opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 (SDR) FAMILY.
 CC EMBL: AE004854; AAC07777.1; -
 DR HSP: P50163; 2AE1.
 DR InterPro: IPR002198; ADH_short.
 DR InterPro: IPR001064; Crystallin.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
 DR Oxidoreductase; Complete proteome.
 KW SEQUENCE 252 AA; 26720 MW; F1F45AB2C2D8DE CRC64;
 SO
 Query Match 27.1%; Score 354; DB 16; Length 252;
 Best Local Similarity 35.1%; Pred. No. 5.6e-17;
 Matches 94; Conservative 40; Mismatches 100; Indels 34; Gaps 7;
 QY 8 VKGLVAVITGASGLGATAEIRLVGOGASAVLLDLPN-----SGEAGAKKLG 55
 DB 3 LKXKVIITGGCGGGRAMGEYLAGARLALVDLNRRLDEAVAAKAGADANA---- 58
 QY 56 NNCVFPADYTSKDVOTLALAKKFGFVDVAVNCAIYAVASKYINLKKGQTH--TLED 113
 DB 59 -----YVCNVADEEQYTHMVAQVAFDGAINGLVNAGITRLDGLITKVGQLSKMSLQ 113
 QY 114 FQRLVDVNLGTFNTVRLVAGEGQ--NEPDGGGGRGVITNTASVAFEGVGOAAYSAS 171
 DB 114 MGSVIDVNLGVEFLCIREVAKKMIELKNE-----GALVNISSISR-AGNMGOANYSA 165
 QY 172 KSGIVMTLPIDAPIGIRVMTAPGLFGTPLTSLPEKYSNFLASQVPPSRIGDPA 231
 DB 166 KAGVADTYVMKELRYGIRVAGVAPGFETEMTGMKPEALEKMTAGIPL-KRMGRV 224
 QY 232 EYAHVQAIENPELNGEYIRLGGAIRM 259
 DB 225 EIAHSVAYIFENDYIRGVLELDGRL 252
 RESULT 21
 Q97DAG PRELIMINARY; PRT; 249 AA.
 ID 097DAG6
 AC 097DAG6
 DT 01-OCT-2001 (TREMBLrel. 18, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE 3-ketoacyl-acyl carrier protein reductase.
 GN CAC3574.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Clostridiales; Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE-21359325; PubMed-11466286;
 RA Moelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Olu D., Hitti J., Wolf Y.I.,
 RA Tatusov R.L., Sadtke E.V., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.,
 RT "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium *Clostridium acetobutylicum*.";
 RL J. Bacteriol. 183:4823-4838(2001).

DR EMBL: AE007854; AAX81497.1; -
 DR InterPro: IPR002198; ADH_short.
 DR InterPro: IPR001092; HH_basic.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
 KW Complete proteome.
 SO SEQUENCE 249 AA; 26247 MW; B13DVEDAC21A626A CRC64;
 Query Match 26.5%; Score 345.5; DB 16; Length 249;
 Best Local Similarity 33.2%; Pred. No. 2.1e-16;
 Matches 86; Conservative 56; Mismatches 96; Indels 21; Gaps 6;
 QY 8 VKGLVAVITGASGLGATAEIRLVGOGASAVLLDLPNSGGEAQ-----ARKLNNCYFAP 62
 DB 5 LSGVAVVATGAGRLGRLAIAKLAEGANLV-VYRSEAEQTKLIEIELGSKAVAK 63
 QY 63 ADVTSKDVOTLALAKKFGFVDVAVNCAIYAVASKYINLKKGQTHITLDFQRYLDVNL 122
 DB 64 ADISKYEAEETIKKALDEGVTDILVNNAGITDNLRLRKE-----EDFQSVINVL 117
 QY 123 MGFNVRLVAGEGQNEPDGGGGRGVITNTASVAFEGVGOAAYSASKGIYGMTLP 182
 DB 118 KGAFNCIKHTRVMLK-----KSGKITINSSVIGLIGNAGOVNVAAGIIGMKSV 171
 QY 183 ARDLAPIGIRVMTAPGLFGTPLTSLPEKYSNFLASQVPPSRIGDPAEYAHVQAIE 242
 DB 172 AKELASRIETVNAVAPGIIKSDMTDALDKOREIVAAPL-NKVGAEADVAVNLPLAS 230
 QY 243 --NPELNGEYIRLGGAIRM 259
 DB 231 DLSITIGQVITNDGGMV 249
 RESULT 22
 Q8R9W PRELIMINARY; PRT; 247 AA.
 ID 08R9W0
 AC 08R9W0
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Dehydrogenases with different specificities (related to short-chain
 DE alcohol dehydrogenases).
 GN FA83 OR TTE1472.
 GN Thermanaerobacter tengcongensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Thermanaerobacteriales; Thermanaerobacteriaceae; Thermanaerobacter.
 OX NCBI_TaxID=119072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MB47 / JCM1007;
 RX MEDLINE-21592816; PubMed-11997336;
 RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
 RA Tan H., Chen R., Wang J., Yu J., Yang H.,
 RT "A complete sequence of *T. tengcongensis* genome.";
 RL Genome Res. 12:689-700(2002).
 DR EMBL: AE013105; AAM24694.1; -
 KW Complete proteome.
 SO SEQUENCE 247 AA; 26606 MW; 357D82B8C60E7947 CRC64;
 Query Match 26.1%; Score 340.5; DB 16; Length 247;
 Best Local Similarity 34.3%; Pred. No. 4.7e-16;
 Matches 87; Conservative 48; Mismatches 100; Indels 19; Gaps 6;
 QY 12 VAVITGASGLGATAEIRLVGOGASAVLLDLPN--SGEAG--QAKKLNKCVFADYTS 67
 DB 7 VAFVIGSGSGIORALAVNLADGFIATYYKDKSABEYEVKKHSHVDALAKCDVSK 66
 QY 68 EKDVTALALAKKFGFVDVAVNCAIYAVASKYINLKKGQTHITLDFQRYLDVNLGTFN 127
 DB 67 YHEVEKAVEKVEEFGSIDVYVNNAGITKNDLILKME-----EEMDQVIDVNLKGAFN 120

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QY 128 VIRIIVAGEMGONNEPDGQSGVITINTASVAAFEGVQQAAYSASKSGITGVMTLPIARDLA 187
DB 121 VIKFASKYMTK-----RKGIITISSVGLMNGVQANVAASKAGITGLTSVAKELA 174
QY 188 PIGIRVMTIAPGLTGPFLTLISLPEKVSNFLASQVFPFSPRLGDPAEVAHLVO--AILENPF 245
DB 175 SRGITVANVAPGFETMTNTVYKDKIDKEAMKLSPL-KRAGKPEVAEVAFLASSASDV 233
QY 246 LNEGVIRLDGAIRM 259
DB 234 ITGQVINVDGGMV 247

RESULT 23
C8YVTO PRELIMINARY: PRT: 251 AA.
AC Q8YVTO.
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase.
GN FARG OR ALR1894.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneo T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriyuchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsuno M., Matsuno A., Mutaki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
DR EMBL: AP003587; BAB73593.1; -
DR InterPro: IPR002198; ADH_short.
DR InterPro: IPR001092; HLH_Dasic.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 251 AA; 26218 MW; 57D0712F8EAB6898 CRC64;

Query Match 25.9%; Score 337.5; DB 16; Length 251;
Best Local Similarity 33.5%; Pred. No. 7,7e-16;
Matches 92; Conservative 45; Mismatches 97; Indels 41; Gaps 7;

QY 1 MAACRSYKGLVAVITGASGLGATAERLVGGASA-----VLDLPRSG 47
DB 1 MAILSENIRGVAVVTGASRGIGRAILELANIYAVVYNASSSTADEVAELTGAGG 60
QY 48 EAQAKKLGNCVFAADVTSEKDYOTALALAKRGFGRVAVVNCAGIYASKTYNLKQG 107
DB 61 EAVALK-----ADVSGVEVDNLINGAIDFKRIDILVNNAGITRDTLLRMKP-- 109
QY 108 THIEDPQRLVDVNLMTGFNIRLVAGEMGONNEPDGQSGVITINTASVAAFEGVQQA 167
DB 110 ----EDWQAVIDLNLTVGLCTRAVSKMLTKQ-----RSGRITNTSVAGQKNGPQAN 159
QY 168 YSASRGGIVMTLPIARDLPIGIRVMTIAPGLTGPFLTLISLPEKVSNFLASQVFPFSPRL 227
DB 160 YSAKAGVIGFTKVAKEIAELASRGITVANVAPGFETMTNTSLK---SEGIIQYIPL-GRY 215
QY 228 GDPAEVAHLVQAILENPF--PLNEGVIRLDGAIRM 259
DB 216 GQPEIAGWRFELADPAALVITQGVFNVDGGMV 250

RESULT 24

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O9KA03
ID O9KA03 PRELIMINARY: PRT: 246 AA.
AC O9KA03;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100).
GN FARG OR BH2491.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis."
RL Nucleic Acids Res. 28:4317-4331(2000).
CC "- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL: AP001515; BAB06210.1; -
DR HSSP: P19992; IHDG.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 246 AA; 26126 MW; 852B95EB8DEB9E90 CRC64;

Query Match 25.8%; Score 336.5; DB 16; Length 246;
Best Local Similarity 34.2%; Pred. No. 8.8e-16;
Matches 90; Conservative 42; Mismatches 102; Indels 29; Gaps 7;

QY 8 VKGLVAVITGASGLGATAERLVGGASAVLDPNSGE-----AQKKKGNVCY 59
DB 2 LQGTIAIVTGASRGIGRAITAMELARGAVV---NAGNKEKERYVAETKEIGVERI 57
QY 60 FAPADVTSEKDYOTALALAKRGFGRVAVVNCAGIYASKTYNLKQGTHTLEDPQRYLD 119
DB 58 AIGADVADSESVQAMVKETIDFGADVILVNNAGITRDLFPRMKE-----EDWDVYID 111
QY 120 VIMGTFNIRLVAGEMGONNEPDGQGR--GVITNTASVAAFEGVQQAAYSASKGIYGM 178
DB 112 TINKGVFHCASKATREPMK-----QREGRIITVSSVGAIGNQAQVYAKAGVIGL 164
QY 179 TPIARDLPIGIRVMTIAPGLTGPFLTLISLPEKVSNFLASQVFPFSPRLGDPAEVAHLVO 238
DB 165 TKLAEELANRNTITVANVAPGFETMTNTSLK---ARLQGEPEVAKAVR 223
QY 239 AILEN--PLNEGVIRLDGAIRM 259
DB 224 FLASDDASYLTGQTHVNGGMV 246

RESULT 25
O42774 PRELIMINARY: PRT: 297 AA.
AC O42774;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase.
GN OAR-1 OR B2A19.180.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.

```

RA Buerger F., Broers B., Weiss H.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Schulte U., Aign V., Hohelsel J., Brandt P., Fartmann B., Holland R.,
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 DR EMBL: AF042860; AAB9799.1; -;
 DR EMBL: AL390092; CAB98248.1; -;
 DR HSSP: 070351; 1E6W;
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Oxidoreductase.
 SQ SEQUENCE 297 AA; 31342 MW; 8DC08FEDF584196F CRC64;

Query Match 25.7%; Score 335.5; DB 3; Length 297;
 Best Local Similarity 31.7%; Pred. No. 1,3e-15;

Matches 97; Conservative 40; Mismatches 102; Indels 67; Gaps 8;

QY 6 RSVKGLVAVITGASGLGATAFRLVGGASAVLDPNS-----GGEAQ 50
 DB 2 RSLHKOALITGGSGGLAARLYLEGCVTLGRTSTLORASQSLLSQPLHSPAQ 61
 QY 51 AKRLGNVCVAPADVTSEKDVOTAL-ALAKGFGVVDVAVNCAGIAVAS--KTYNLKRG 106
 DB 62 QPSDTRKVSHPPLNVTSASWEDLDSNSGKGRVDILNCAGITQRSPLMKT----- 115
 QY 107 QHTLEDFOFRLDVNIMGTFNVIRLVAGENGQNEP-----DOG- 145
 DB 116 --SIEVEGLIDTLNLTGCKFVGRAMLNRRPSQHPRVKADDEGAGVWEGTEEG 172
 QY 146 -----ORGVIINTASVAFAEGOVGOAAYSASKGIYGMTLPIDRLAPIGI 191
 DB 173 KGGKGGVREGVGEQGVIIINVASLAKQCVIGTSYAAAKAGVGLTSLAHEYGRSGI 232
 QY 192 RVNMTIABGLFGTPLLTLSPKVSNTLASQVPPPSRLGDPAEYAHIVQAITENPFLNGEVI 251
 DB 233 RVNAVYLPGYIETIMTGLK---NPSIIQCIPL-GRFGTDEVADALFLIKNPYANNCVL 288
 QY 252 RLDDGI 257
 DB 289 NLDDGL 294

Search completed: June 23, 2003, 14:32:49
 Job time : 32.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:19:47 ; Search time 7.8333 Seconds
(without alignments)
1381.936 Million cell updates/sec

Title: US-09-931-186-23

Perfect score: 1304

Sequence: 1 MAACRSVKGGLVAVITGGAS.....ENPFLNGEVIRLDGARIMQP 261

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1299	99.6	261	1	HCD2_HUMAN
2	1208	92.6	261	1	HCD2_BOVIN
3	1153	88.4	260	1	HCD2_RAT
4	1134	87.0	261	1	HCD2_MOUSE
5	910	63.8	255	1	HCD2_DROME
6	382.5	29.3	247	1	Y050_MYCTU
7	343	26.3	246	1	FABG_THENA
8	338	25.9	320	1	FABG_CUPLA
9	331.5	25.4	261	1	DHB8_HUMAN
10	330.5	25.3	244	1	FABG_VIBCH
11	316.5	24.3	260	1	DHB8_MOUSE
12	312.5	24.0	246	1	FABG_BACSU
13	305	23.4	260	1	FAG1_SYNT3
14	304	23.3	255	1	YK02_MYCTU
15	302	23.2	255	1	YMPD_BACSU
16	296.5	22.7	244	1	2BHD_STREX
17	296.5	22.5	244	1	YAYI_RHISN
18	293.5	22.5	244	1	FABG_VIBHA
19	293.5	22.5	244	1	FABG_AQUAE
20	291.5	22.4	244	1	FABG_ECOLI
21	291	22.3	249	1	BAV1_EUBSP
22	287	22.0	263	1	UCPA_SALTY
23	286.5	22.0	246	1	P4HB_AICEU
24	285.5	21.9	244	1	FABG_SALTY
25	285.5	21.9	256	1	Y019_THEMA
26	285	21.9	248	1	PHAB_AICIS
27	283.5	21.7	246	1	NODG_AICIS
28	283	21.7	259	1	CMTR_PSEPU
29	282.5	21.7	248	1	FABG_CHIMU
30	279	21.4	250	1	LINC_PSEPA
31	278.5	21.4	241	1	PHAB_ZOORA
32	277	21.2	246	1	PHAB_CHRVT
33	276.5	21.2	289	1	YHDF_BACSU

34	276	21.2	249	1	BA72_EUBSP
35	276	21.2	319	1	FABG_ARATH
36	275	21.1	263	1	UCPA_ECO57
37	275	21.1	263	1	UCPA_ECOLI
38	273.5	21.0	247	1	FABG_CHLIR
39	272.5	20.9	240	1	FAG2_SYNT3
40	271	20.8	250	1	LINC_PSEPA
41	271	20.8	251	1	Y325_THEMA
42	269.5	20.7	242	1	FABG_HAEIN
43	269.5	20.7	262	1	DHB8_HAEIN
44	268.5	20.6	261	1	DHR8_STRCM
45	267	20.5	347	1	FABG_MYCTU
46	266.5	20.4	236	1	TS2_MAIZE
47	265.5	20.4	241	1	P4HB_RHIME
48	262	20.1	256	1	BUDC_KLEPN
49	262	20.1	261	1	DHGA_BACME
50	261	20.0	258	1	DHG2_BACSU
51	260	19.9	261	1	DHG3_BACME
52	260	19.9	261	1	DHG2_BACME
53	259	19.9	261	1	YOXD_BACSU
54	258.5	19.8	238	1	DHG4_BACME
55	258	19.8	261	1	DHG1_BACME
56	257	19.7	261	1	FABG_RICPR
57	256.5	19.7	241	1	DHG3_BACSU
58	255	19.6	261	1	DHG2_BACSU
59	254.5	19.5	263	1	PGDH_HUMAN
60	252	19.3	256	1	Y4MP_RHISN
61	251.5	19.3	261	1	ACT3_STRCO
62	251.5	19.3	267	1	SORD_KLEPN
63	250.5	19.2	253	1	3BHD_COMTE
64	249.5	19.1	285	1	YXHC_BACSU
65	247.5	19.0	245	1	NODG_RHIS3
66	247	18.9	256	1	GNO_GLOOX
67	244.5	18.8	262	1	YXBG_BACSU
68	244	18.7	255	1	YV06_PSEAE
69	243	18.6	255	1	HDHA_ECOLI
70	243	18.5	270	1	DHMA_PLASI
71	241.5	18.5	258	1	BDHA_RHIME
72	241	18.5	255	1	FABG_MYCAT
73	240.5	18.4	261	1	YGCW_ECOLI
74	240	18.4	247	1	FABG_PSEAE
75	240	18.4	248	1	FABG_CHLIP
76	239	18.3	257	1	YXJF_BACSU
77	232.5	17.8	245	1	NODG_RHIME
78	229.5	17.6	273	1	TRN1_DATST
79	228.5	17.6	894	1	FOX2_NEUCR
80	228.5	17.5	249	1	DHK2_STEVN
81	228.5	17.5	258	1	BDHA_ALCEU
82	226	17.3	254	1	IDNO_ECOLI
83	225.5	17.3	242	1	PHAB_PARDE
84	225.5	17.3	256	1	DH80_RHOSH
85	225	17.3	255	1	FABG_MYCSM
86	224.5	17.2	256	1	MTDH_UROPA
87	223.5	17.1	259	1	SRUD_ECOLI
88	223	17.1	241	1	BUDC_KLETE
89	222.5	17.0	900	1	FOX2_YEAST
90	221.5	17.0	253	1	KDUD_ECOLI
91	221.5	17.0	272	1	DHK1_STEVN
92	221	16.9	254	1	KDUD_BACSU
93	220.5	16.9	285	1	GS39_BACSU
94	219	16.8	248	1	V452_LISIN
95	215	16.5	242	1	FABG_ACTRA
96	214.5	16.4	286	1	YAY8_SCHPO
97	214	16.4	299	1	YAXD_BACSU
98	213.5	16.4	278	1	YALA_RHISN
99	213	16.3	134	1	DHB8_CALVA
100	213	16.3	248	1	V432_LISMO

ALIGNMENTS

P19337 eubacterium
P33207 arabidopsis
O8b14 escherichia
P37440 escherichia
P38004 chlamydia t
P73826 synechocyst
P50198 pseudomonas
Q9w90 thermotoga
P43713 haemophilus
P07999 bacillus me
P41177 streptomyces
Q4830 mycobacteri
P50160 zea mays (m
P50205 rhizobium m
Q48436 klebsiella
P10528 bacillus me
P80869 bacillus su
P39484 bacillus me
P40288 bacillus me
P39483 bacillus me
P14902 bacillus su
P39485 bacillus me
P39482 bacillus me
P50941 rickettsia
P12310 bacillus su
P15428 homo sapien
P55575 rhizobium s
P16544 streptomyces
P37079 klebsiella
P19871 comamonas t
P40397 bacillus su
P72332 rhizobium s
P50139 gluconobact
F4631 bacillus su
Q51576 pseudomonas
P25599 escherichia
P22441 flavobacter
O86034 rhizobium m
O07399 mycobacteri
P76633 escherichia
O54438 pseudomonas
Q928P2 chlamydia p
P42317 bacillus su
P06234 rhizobium m
P50162 datura stra
O01373 neurospora
P16543 streptomyces
Q9w612 alcaligenes
P39435 escherichia
P50204 paracoccus
P50204 paracoccus
Q59787 rhodobacter
P71534 mycobacteri
O00058 urmyces fa
P05707 escherichia
O45574 klebsiella
Q02207 saccharomyc
P37769 escherichia
P50842 streptomyces
P50842 bacillus su
O92267 bacillus su
P70720 actinobactil
Q10238 schistosach
P50338 bacillus su
Q55541 rhizobium s
Q9w613 callithrix
P25145 listeria me

HCD2_HUMAN STANDARD; PRT; 261 AA.

AC Q99714; 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)

DE (Endoplasmic reticulum-associated amyloid beta-peptide binding protein) (Short-chain type dehydrogenase/reductase XH98G2).

GN HADH2 OR ERH2 OR XH98G2 OR SCHAD.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RA MEDLINE=97478528; PubMed=9338779;

RA Yan S.D., Fu J., Soto C., Chen X., Zhu H., Al-Mohanna F., Collins K., Zhu A., Stern E., Saldo T., Tohyama M., Ogawa S., Rohrer A., Stern D.

RA "An intracellular protein that binds amyloid-beta peptide and mediates neurotoxicity in Alzheimer's disease."

RT Nature 389:689-695(1997).

RL [2]

RP SEQUENCE FROM N.A.

RA Zhuchenko O.P., Wehnert M., Bailey J., Sun Z.S., Lee C.C.; Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

RL [3]

RP SEQUENCE FROM N.A.

RA MEDLINE=98337980; PubMed=9671743;

RA Miller A.P., Willard H.F.;

RA "Chromosomal basis of X chromosome inactivation: Identification of a multigene domain in Xp11.21-p11.22 that escapes X inactivation."

RL Proc. Natl. Acad. Sci. U.S.A. 95:8709-8714(1998).

RL [4]

RP SEQUENCE FROM N.A.

RA TISSUE=Brain;

RA MEDLINE=98221216; PubMed=9553139;

RA He X.Y., Schulz H., Yang S.Y.;

RA "A human brain L-3-hydroxyacyl-coenzyme A dehydrogenase is identical to an amyloid beta-peptide-binding protein involved in Alzheimer's disease."

RL J. Biol. Chem. 273:10741-10746(1998).

RL [5]

RP SEQUENCE FROM N.A.

RA TISSUE=Lung;

RA Strausberg R.;

RA Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

RL -1- FUNCTION: BINDS INTRACELLULAR AMYLOID-BETA. BY INTERACTING WITH AMYLOID-BETA, IT MAY CONTRIBUTE TO THE NEURONAL DYSFUNCTION ASSOCIATED WITH ALZHEIMER DISEASE.

CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA + NADH.

CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

CC -1- TISSUE SPECIFICITY: EXPRESSED IN NORMAL TISSUES BUT IS OVEREXRESSED IN NEURONS AFFECTED IN AD.

CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.

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CC EMBL; U96132; AAC51812.1; -

CC EMBL; U73514; AB68581.1; -

CC EMBL; AF069134; AAC39900.1; -

CC EMBL; AF035555; AAC15902.1; -

CC EMBL; AF037438; AAC16419.1; -

DR EMBL; BC000372; AAH00372.1; -

DR HSSP; 070351; 1E3S.

DR Genew; HGNC:4600; HADH2.

DR MIM; 300256; -

DR InterPro; IPR02198; ADH_short.

DR Pfam; PF00106; adh_short; 1.

DR PRINTS; PR00080; SDRFAMILY.

DR PROSITE; PS00061; ADH_SHORT; 1.

KW Oxidoreductase; NAD.

FT NP_BIND 12 37 NAD (BY SIMILARITY).

FT ACT_SITE 168 168 BY SIMILARITY.

SO SEQUENCE 261 AA; 26923 MW; 9E74F242E3E6E9F1 CRC64;

Query Match 99.6%; Score 1399; DB 1; Length 261;

Best Local Similarity No. 4.3e-93;

Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAARSVKGLAVITGASGIGTAFARLVGGASAVLLDLPNSGGEPAOKKIGNCVF 60

DB 1 MAAARSVKGLAVITGASGIGTAFARLVGGASAVLLDLPNSGGEPAOKKIGNCVF 60

QY 61 APADYTSKDVOTATLAKGKFGKRVAVNCAGIYASRTYLNKKGTHTLEDFORVLDV 120

DB 61 APADYTSKDVOTATLAKGKFGKRVAVNCAGIYASRTYLNKKGTHTLEDFORVLDV 120

QY 121 NLMGFNVRILVAGENGQNEPDGQGVITNTASVAFEGVGQAASASRGGVGTLL 180

DB 121 NLMGFNVRILVAGENGQNEPDGQGVITNTASVAFEGVGQAASASRGGVGTLL 180

QY 181 PIARDIAPIGIRVMTIAPLFGTPLTSLPEKVSNFLASQVFPSPRLDPAEYATLVQAI 240

DB 181 PIARDIAPIGIRVMTIAPLFGTPLTSLPEKVSNFLASQVFPSPRLDPAEYATLVQAI 240

QY 241 IENPFLNGEYIRLDGAIKRP 261

DB 241 IENPFLNGEYIRLDGAIKRP 261

RESULT 2

HCD2_BOVIN STANDARD; PRT; 261 AA.

AC Q02651; 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH).

GN HADH2.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE=Liver;

RA MEDLINE=97214648; PubMed=9061028;

RA Furuta S., Kobayashi A., Miyazawa S., Hashimoto T.;

RT Cloning and expression of cDNA for a newly identified isozyme of bovine liver 3-hydroxyacyl-CoA dehydrogenase and its import into mitochondria."

RL Biochim. Biophys. Acta 1350:317-324(1997).

CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA + NADH.

CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Mitochondrial.

CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.

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CC -----

DR EMBL: AB002156; BAA19510.1; -

DR HSPB: 070351; 1E6W.

DR InterPro: IPR002198; ADH_short.

DR Pfam: PF00106; adh_short; 1.

DR PRINTS: PR00080; SDRFAMILY.

DR PROSITE: PS00061; ADH_SHORT; 1.

KW Oxidoreductase; NAD; Mitochondrion.

FT NP_BIND 12 37 NAD (BY SIMILARITY).

FT ACT_SITE 168 168 BY SIMILARITY.

SQ SEQUENCE 261 AA; 27140 MW; 8C7572B6A9A49780 CRC64;

Query Match 92.6%; Score 1208; DB 1; Length 261;

Best Local Similarity 92.0%; Pred. No. 4.3e-86;

Matches 240; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 MAACRSYKGLVAVITGASGLGATLAEKRLVGGASAVLLDLENSGGEAQAALGNVCYF 60

DB 1 MAACRSYKGLVAVITGASGLGATLAEKRLVGGASAVLLDLENSGGEAQAALGNVCYF 60

QY APADVTSEKDVQATLALAKGKFGVDVAVNCAGIAVASKTYNKKGGTHTLEDFORVLDV 120

DB 61 APADVTSEKDVQATLALAKGKFGVDVAVNCAGIAVASKTYNKKGGTHTLEDFORVLDV 120

QY 121 NMGTENVIRLVAGEQONBPDGOGGQGVIIINTASVAEFGVGOQAAYSASKGGIVGNTL 180

DB 121 NMGTENVIRLVAGEQONBPDGOGGQGVIIINTASVAEFGVGOQAAYSASKGGIVGNTL 180

QY 121 NLITFNVIRLVAGEQONBPDGOGGQGVIIINTASVAEFGVGOQAAYSASKGGIVGNTL 180

DB 181 PIARDLAPIGIRVWTIPAGLFGPPLTSLPEKYSNFIASQVPPSRIGDPAEYAHLYQAT 240

QY 181 PIARDLAPIGIRVWTIPAGLFGPPLTSLPEKYSNFIASQVPPSRIGDPAEYAHLYQAT 240

DB 241 IENPFLNGEVIIRLDGAIKMP 261

QY 241 IENPFLNGEVIIRLDGAIKMP 261

DB 241 IENPFLNGEVIIRLDGAIKMP 261

RESULT 3

HCD2_RAT

ID HCD2_RAT STANDARD; PRT; 260 AA.

AC 070351; Q8QYD4;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)

DE (Endoplasmic reticulum-associated amyloid beta-peptide binding protein).

GN HADH2 OR ERAB.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OC NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RP TISSUE=Liver;

RA "Rattus norvegicus amyloid beta-peptide binding protein (ERAB) mRNA."

RT Submitted (FEB-1998) to the EMBL/Genbank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RP STRAIN=Sprague-Dawley; TISSUE=Brain;

RA Yang S.-Y., He X.-Y.;

RT "Molecular cloning and characterization of the cDNA of rat brain short chain L-3-hydroxyacyl-CoA dehydrogenase."

RT Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.

RN [3]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RP TISSUE=Brain;

RC MEDLINE=20481418; PubMed=11023795;

RA Powell J.A., Read J.A., Banfield M.J., Gunn-Moore F., Yan S.D., Lustbader J., Stern A.R., Stern D.M., Brady R.L.;

RT "Recognition of structurally diverse substrates by type II 3-hydroxyacyl-CoA dehydrogenase (HADH II)/amyloid-beta binding protein."

RT J. Mol. Biol. 303:311-327(2000).

CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA + NADH.

CC -1- SUBUNIT: HOMOTETRAMER.

CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).

CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDOUCTASES (SCR) FAMILY.

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CC -----

DR EMBL: AF048878; AAC05747.1; -

DR EMBL: AF069770; AAF14853.1; -

DR PDB: 1E3W; 25-MAY-01.

DR PDB: 1E3S; 25-MAY-01.

DR PDB: 1E6W; 25-MAY-01.

DR InterPro: IPR002198; ADH_short.

DR Pfam: PF00106; adh_short; 1.

DR PRINTS: PR00080; SDRFAMILY.

DR PROSITE: PS00061; ADH_SHORT; 1.

KW Oxidoreductase; NAD; Acetylation; 3D-structure.

FT INIT_MET 0 0 BY SIMILARITY.

FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).

FT NP_BIND 11 36 NAD (BY SIMILARITY).

FT ACT_SITE 167 167 BY SIMILARITY.

FT CONFLICT 4 4 V -> C (IN REF. 2)

SQ SEQUENCE 260 AA; 27114 MW; 30E7E73A95F9227 CRC64;

Query Match 88.4%; Score 1153; DB 1; Length 260;

Best Local Similarity 87.7%; Pred. No. 7.3e-82;

Matches 228; Conservative 17; Mismatches 15; Indels 0; Gaps 0;

QY 2 MAACRSYKGLVAVITGASGLGATLAEKRLVGGASAVLLDLENSGGEAQAALGNVCYF 61

DB 1 MAACRSYKGLVAVITGASGLGATLAEKRLVGGASAVLLDLENSGGEAQAALGNVCYF 60

QY 62 PADVTSEKDVQATLALAKGKFGVDVAVNCAGIAVASKTYNKKGGTHTLEDFORVLDV 121

DB 61 PADVTSEKDVQATLALAKGKFGVDVAVNCAGIAVASKTYNKKGGTHTLEDFORVLDV 120

QY 122 NMGTENVIRLVAGEQONBPDGOGGQGVIIINTASVAEFGVGOQAAYSASKGGIVGNTL 181

DB 122 NMGTENVIRLVAGEQONBPDGOGGQGVIIINTASVAEFGVGOQAAYSASKGGIVGNTL 180

QY 121 NLITFNVIRLVAGEQONBPDGOGGQGVIIINTASVAEFGVGOQAAYSASKGGIVGNTL 180

DB 182 IARDLAPIGIRVWTIPAGLFGPPLTSLPEKYSNFIASQVPPSRIGDPAEYAHLYQAT 241

QY 181 IARDLAPIGIRVWTIPAGLFGPPLTSLPEKYSNFIASQVPPSRIGDPAEYAHLYQAT 240

DB 242 IENPFLNGEVIIRLDGAIKMP 261

QY 242 IENPFLNGEVIIRLDGAIKMP 260

DB 241 IENPFLNGEVIIRLDGAIKMP 260

RESULT 4

HCD2_MOUSE

ID HCD2_MOUSE STANDARD; PRT; 261 AA.

AC 008756;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)

DE (Endoplasmic reticulum-associated amyloid beta-peptide binding protein).

GN HADH2 OR HSD17B10 OR ERAB.

OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN=C57BL/6 X CBA;
 CC Fu J., Chen X., Stern D., Yan S.D.;
 CC Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA
 CC + NADH.
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL; U96116; AAB57689.1; ALT_INIT.
 CC DR HSSP; 070351; 1B6W.
 CC DR SWISS-2DPAGE; 008756; MOUSE.
 CC DR MGD; MGI:133871; Hsd17b10.
 CC DR InterPro: IPR002198; ADH_short.
 CC DR Pfam: PF00106; adh_short; 1.
 CC DR PRINTS: PR00080; SDRFAMILY.
 CC DR PROSITE; PS00061; ADH_SHORT; 1.
 CC KM Oxidoreductase; NAD.
 CC FT NP_BIND 12 37 NAD (BY SIMILARITY).
 CC FT ACT_SITE 168 168 BY SIMILARITY.
 CC SQ SEQUENCE 261 AA; 27418 MW; 61213B13E2839D41 CRC64;

Query Match 87.0%; Score 1134; DB 1; Length 261;
 Best Local Similarity 86.2%; Pred. No. 2.1e-80;
 Matches 225; Conservative 19; Mismatches 17; Indels 0; Gaps 0;
 QY 1 MAACRSYKGLVAVITGSGASGLGATLAEVLVGQGSASVLLDLPSSGGEAQAQKLGNCVE 60
 DB 1 MAAVRSYKGLVAVITGSGASGLGATLAEVLVGQGSASVLLDLPSSGGEAQAQKLGNCVE 60
 QY 61 APADVTSEKDVQATALAKKGFGRVDVAVNAGAVASKTYNNLKKGQTHLEDRVLVD 120
 DB 61 APADVTSEKDVQATALAKKGFGRVDVAVNAGAVASKTYNNLKKGQTHLEDRVLVD 120
 QY 121 NLMGTFNFIKLVAGMGONERPDGQGRVYINTASVAAFEQGVCAQAYSASAKGIVAKTL 180
 DB 121 NLMGTFNFIKLVAGMGONERPDGQGRVYINTASVAAFEQGVCAQAYSASAKGIVAKTL 180
 QY 181 PIARDLPIGIRVMTIAPGLFGTPLLISLPKVSNTLASQVPEPSRLGDPREVAHLVQAI 240
 DB 181 PIARDLPIGIRVMTIAPGLFGTPLLISLPKVSNTLASQVPEPSRLGDPREVAHLVQAI 240
 QY 241 IENPPLNGEVIKLDGAIKMP 261
 DB 241 IENPPLNGEVIKLDGAIKMP 261

RESULT 5

HSD2_DROME STANDARD; PRT; 255 AA.

AC 018404;
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)
 DE (Scully protein).
 GN SCU OR CG7113.
 OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

CC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 CC NCBI_TaxID=7227;
 CC [1]
 CC SEQUENCE FROM N.A., AND MUTAGENESIS OF LEU-33 AND PRE-120.
 CC STRAIN=Canon-S;
 CC MEDLINE=98252652; PubMed=9585418;
 CC Torroja L., Ortuno-Sanagu D., Ferrus A., Hemmerle B., Barbas J.A.;
 CC "Scully", an essential gene of Drosophila, is homologous to mammalian
 CC mitochondrial type II L-3-hydroxyacyl-CoA dehydrogenase/amyloid-beta
 CC peptide-binding protein.";
 CC J. Cell Biol. 141:1009-1018(1998).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC STRAIN=Berkeley;
 CC MEDLINE=20196006; PubMed=10731132;
 CC Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 CC Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 CC George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 CC Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 CC Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
 CC Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 CC Anil J.F., Agbayani A., An H.-J., Andrews-Frannkoc C., Baldwin D.,
 CC Ballow R.M., Basu N.V., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 CC Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 CC Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 CC Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 CC Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 CC de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 CC Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunker B.C., Dunn P.,
 CC Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
 CC Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 CC Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 CC Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 CC Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwa C.,
 CC Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 CC Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 CC Lascko P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 CC Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 CC Merkulov G., Mitsuhashi N.V., Modarri C., Morris J., Mostrel A.,
 CC Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 CC Nelson D.R., Nelson K.A., Nixon K., Nusslein D.R., Pacle J.M.,
 CC Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 CC Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 CC Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 CC Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 CC Sytkas R., Teclor C., Turner R., Venter E., Wang A.H., Wang X.,
 CC Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 CC Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 CC Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 CC Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 CC Gibbs R.A., Myers E.W., Rubin G.M., Venter T.C.;
 CC "The genome sequence of Drosophila melanogaster.";
 CC Science 287:2185-2195(2000).
 CC -1- FUNCTION: MAY PLAY A ROLE IN GERM LINE FORMATION.
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA
 CC + NADH.
 CC -1- SUBUNIT: MULTIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
 CC -1- TISSUE SPECIFICITY: FOUND IN MANY TISSUES INCLUDING CNS. HIGHEST
 CC EXPRESSION IN BOTH EMBRYONIC GONADAL PRIMORDIA AND MATURE OVARIES
 CC AND TESTES.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
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 CC -----
 CC EMBL; Y15102; CA95377.1; -

DR EMBL: AE003507; AAF48797.1; -
 DR HSSP: 070351; 1E6W;
 DR FlyBase: FBgn0021765; scu.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PRO0080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Oxidoreductase; NAD; Mitochondrion.
 FT NE_BIND 6 NAD (BY SIMILARITY).
 FT ACT_SITE 162 162 BY SIMILARITY.
 FT MOTAGEN 33 L->Q: LEITHAL ALLELE.
 FT MOTAGEN 120 F->I: LEITHAL ALLELE.
 SQ SEQUENCE 255 AA; 26905 MW; F58690643FA0FD03 CRC64;

Query Match 69.8%; Score 910; DB 1; Length 255;
 Best Local Similarity 68.9%; Pred. No. 3.5e-63;
 Matches 175; Conservative 29; Mismatches 50; Indels 0; Gaps 0;

QY 8 VKGIYAVITGASGLGIAETAEIVGQASAVYLDLPNSGGEQAQKLGNNCFAPADYTS 67
 DB 2 IKNAVSLVTGASGLGIAETAEIVGQASAVYLDLPSSKNGEVAKELGDKVVPVADYTS 61
 QY 68 EKDVOYALAIKAGKFGVAVVAVNCAGIAVASKYVNLKGGTHTLEDFQVLDVNLGFTN 127
 DB 62 EKDVSAALQTAQKKEFGRLDVTNCAGIATVAKTFENKKNVAHLEDFQVRLNINVTGEN 121
 QY 128 VIRLVAGMGONEDPGGQGVYIINTASVAFEGVQAAVSAKSGIYGMTLPIDADLS 187
 DB 122 VIRLSAGLMGANENPGQGVYIINTASVAFEGVQAAVSAKSGIYGMTLPIDADLS 181
 QY 188 PIGIRVMTIAPGLTGPLTSLPEKVSNTLASQVPPPSRLGDPAEVAHLVQAIITENPFLN 247
 DB 182 TQGRICITIAAGLENTFMALPEKVTFTFLAKSIPEQRIGSESEVAHLVQAIITENPFLN 241
 QY 248 GEVIRIDGAIKMP 261
 DB 242 GEVIRIDGAIKMP 255

RESULT 6
 YD50_MYCTU STANDARD; PRT; 247 AA.
 ID YD50_MYCTU
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Putative oxidoreductase Rv1350 (EC 1.-.-.-).
 GN FABG2 OR Rv1350 OR MT1393 OR MTCY02B10.14.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetalia; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37Rv;
 RC MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Kiehl J., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sultun J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Bisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,

RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.,
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains."
 RL Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC
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CC EMBL: Z75555; CA99983.1; -
 CC EMBL: AE007012; AAK45656.1; -
 DR HSSP: 070351; 1E3S.
 DR TIGR: MT1393; -
 DR TubercuList: Rv1350; -
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PRO0080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
 FT NE_BIND 9 NAD (BY SIMILARITY).
 FT ACT_SITE 155 155 BY SIMILARITY.
 SQ SEQUENCE 247 AA; 25871 MW; 76CA07892E7BBA73 CRC64;

Query Match 29.3%; Score 382.5; DB 1; Length 247;
 Best Local Similarity 38.9%; Pred. No. 1.3e-22;
 Matches 96; Conservative 43; Mismatches 91; Indels 17; Gaps 5;

QY 13 AVITGASGLGIAETAEIVGQASAVYLDLPNSGGEQAQKLGNN-CYFAPADYTSKD 70
 DB 10 AVITGASGLGIAETAEIVGQASAVYLDLPNSGGEQAQKLGNN-CYFAPADYTSKD 69
 QY 71 VOTLALAKGKGRVDVAVVAVNCAGIAVASKYVNLKGGTHTLEDFQVLDVNLGFTN 130
 DB 70 VDLIRTAVEREGDLMVNNAGITDADM-----RTMEQDFDVIAHLKGTN 123
 QY 131 LVAGMGONEDPGGQGVYIINTASVAFEGVQAAVSAKSGIYGMTLPIDADLS 190
 DB 124 LAALAKRER-----KRGAIYNNSSVSGKGVNMTYSAKAGIYGMTKAAKELAHG 177
 QY 191 IRVMTIAPGLTGPLTSLPEKVSNTLASQVPPPSRLGDPAEVAHLVQAIITENPFLN 248
 DB 178 IRVNAIAPGLIRSNTEAMFQRIWDKLEVPW-GRAGSESEVAHLVQAIITENPFLN 236
 QY 249 EVIRIDG 255
 DB 237 TVLDYTG 243

RESULT 7
 FABG_THEME STANDARD; PRT; 246 AA.
 ID FABG_THEME
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 3-oxoacyl-l-acyl-carrier protein reductase (EC 1.1.1.100) (3-ketoacyl-
 DE acyl carrier protein reductase).
 GN FABG OR TM1724.
 OS Thermotoga maritima.
 OC Bacteria; Thermotogae; Thermotogae (class); Thermotogales;
 OC Thermotogaceae; Thermotoga.
 OX NCBI_TaxID=2336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSB / DSM 3109;
 RC MEDLINE=99287316; PubMed=10360571;

RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
 RA Hatt D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Utterback T.R., Malek J.A., Linher R.C., Garrett M.M.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.:
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 RT genome sequence of *Thermococcus maritima*.";
 RL Nature 399:323-329(1999).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AE001811; AAD36790.1; .
 DR HSSP: P50162; IAE1.
 DR TIGR: TML724; .
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR Fatty acid biosynthesis: Oxidoreductase; NADP. Complete proteome.
 KW NP_BIND 10 34 NADP (BY SIMILARITY).
 FT ACET_SITE 154 154 BY SIMILARITY.
 FT SEQUENCE 246 AA; 26401 MW; 8C08904D28099142 CRC64;
 SQ
 Query Match 26.3%; Score 343; DB 1; Length 246;
 Best Local Similarity 33.7%; Pred. No. 1,4e-19;
 Matches 86; Conservative 47; Mismatches 104; Indels 18; Gaps 5;
 QY 8 VKGLAVITGASGLGATFAERLVGGASAVLLDLPNSGGEA---QAKRLGNCVFAPAD 64
 DB 3 LEGVCLITGAASIGKATILLFPAQEGATVIADISKENDSLYKKEAGLPKAVDPTVLN 62
 QY 65 VTSKDVQFALALAKGFRGVAVANCAGIYAVSKTYNLKGGQTHLEDFQRYLVNLMG 124
 DB 63 VTDDQIKVEYKVEKVGKGRIDVLYNNAIGTRDALVLMKE-----EDMDAVINVLKG 116
 QY 125 TENYIRLVAGEMGNEPDGQGRVVIINTASVAFBEQVQGAAYASAKSGIYGMLEPIAR 164
 DB 117 VFNVTQNVFPMIQ-----KNSIVSVSSVGIYINPGQTVYAAKAGVITGMKTWAK 170
 QY 185 DLADIGIRVMTIADGEGTPLLTLSPKVSNFLASQVFPFSLGDPAPAYALV--QALIE 242
 DB 171 ELAQRNIRVNAVAGFETLPTKTLPEKARETALSRLPL--GREGKPREVAQVILFLASDE 229
 QY 243 NPELNGEYIRLDGAI 257
 DB 230 SYVTGVIGIDGGL 244

OC Spermatohyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosides II; Myrtales; Lythaceae; Cuphea.
 OX NCBI_Taxid=3930;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92293104; PubMed=1376402;
 RA Klein B., Pawlowski K., Hoeicke-Grandpierre C., Schell J.,
 RA Toepfer R.:
 RT "Isolation and characterization of a cDNA from *Cuphea lanceolata*
 RT encoding a beta-ketoacyl-ACP reductase.";
 RL Mol. Gen. Genet. 233:122-128(1992).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.
 CC -1- SUBUNIT: HOMOTETRAMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST AND NON-PHOTOSYNTHETIC
 CC PLASTIDS.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X64566; CAA45866.1; .
 DR PIR: S19832; S19832.
 DR HSSP: P50162; IAE1.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR Fatty acid biosynthesis: Oxidoreductase; NADP; Chloroplast;
 KW Transil peptide.
 FT TRANSIT 1 61
 FT CHAIN 62 320
 FT NP_BIND 82 106 CHLOROPLAST (BY SIMILARITY).
 FT ACET_SITE 227 227 3-OXOACYL-[ACYL-CARRIER PROTEIN]
 FT SEQUENCE 320 AA; 33103 MW; 06BAF052282B8C87 CRC64;
 SQ
 Query Match 25.9%; Score 338; DB 1; Length 320;
 Best Local Similarity 32.7%; Pred. No. 4,6e-19;
 Matches 87; Conservative 47; Mismatches 110; Indels 22; Gaps 6;
 QY 2 AAACRKYKLAVITGASGLGATFAERLVGGASAVLLDLPNSGGEA---QAKRLGNC 56
 DB 69 AGAGQSVESPVVITVAGSGIGKATILLFPAQEGATVIADISKENDSLYKKEAGLPKAVDPTVLN 127
 QY 57 NCFAPADVTSEKDVQFALALAKGFRGVAVANCAGIYAVSKTYNLKGGQTHLEDFQRYLVNLMG 116
 DB 128 QALTEGQDVSKEDVYAMIKTAVDAMGTVDILYNNAGITRDGLLMKMKSC-----WQE 181
 QY 117 VLDVNLMTGFNNIRLVAGEMGNEPDGQGRVVIINTASVAFBEQVQGAAYASAKSGIY 176
 DB 182 VIDLNTGVFLCTQAAAKIMKK-----KKRIINIASVGLVGNAGQANTSAKAGVIT 235
 QY 177 GMTLPFARDLAPIGIRVMTIADGEGTPLLTLSPKVSNFLASQVFPFSLGDPAPAYALV 236
 DB 236 GFTKYARARYASANNIVNAVAPGISSDMTSLGDDINKKILLETIPL--GRYGQPREVAVGL 294
 QY 237 VQALIEP---FLNGEYIRLDGAI 259
 DB 295 VERLAINPASSVYTGQVFTIDGGM 320

RESULT 9
 DHB8_HUMAN
 ID DHB8_HUMAN STANDARD; PRT; 261 AA.

AC Q92506; Q9UIQ1;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Estradiol 17 beta-dehydrogenase 8 (EC 1.1.1.62) (17-beta-HSD 8) (17-
 beta-hydroxysteroid dehydrogenase 8) (K6 protein) (K6-6).
 GN HSD17B8 OR HKE6 OR RING2 OR FABG.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tubby B.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 3-261 FROM N.A.
 RX MEDLINE=97001166; PubMed=8812499;
 RA Ando A., Kikuchi Y.Y., Shigenari A., Kawata H., Okamoto N., Shitina T.,
 Chen L., Ikemura T., Abe K., Kimura M., Inoko H.;
 RT "cDNA cloning of the human homologues of the mouse K6 and K6 genes
 at the centromeric end of the human MHC region.";
 RL Genomics 35:600-602(1996).
 CC -1- FUNCTION: USES ESTRADIOL AS ITS PREFERRED SUBSTRATE.
 CC -1- CATALYTIC ACTIVITY: Estradiol-17-beta + NAD(P)(+) = estrone +
 NAD(P)H.
 CC -1- PATHWAY: BIOSYNTHESIS OF ESTROGENS.
 CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN THE LIVER AND PANCREAS,
 LOWER IN THE SKELETAL MUSCLE AND KIDNEY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 (SDR) FAMILY.
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 CC -----
 DR EMBL: AL031228; CAC38444.1; -;
 DR EMBL: D82061; BA01529.1; -;
 DR HSSP: 070351; 1E6W.
 DR GeneW: HGNC:3554; HSD17B8.
 DR MIM: 601417; -;
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KM Steroid biosynthesis; Oxidoreductase; NAD; Multigene family.
 FT NP_BIND 15 39 NAD (BY SIMILARITY).
 FT ACT_SITE 169 169 BY SIMILARITY.
 FT CONFLICT 117 117 E -> R (IN REF. 2).
 FT CONFLICT 193 193 R -> P (IN REF. 2).
 FT CONFLICT 208 208 Q -> K (IN REF. 2).
 FT CONFLICT 212 212 Q -> K (IN REF. 2).
 SQ SEQUENCE 261 AA; 26574 MW; 888B2D731714D71 CRC64;
 Query Match 25.4%; Score 331.5; DB 1; Length 261;
 Best Local Similarity 31.2%; Pred. No. 1,1e-18;
 Matches 83; Conservative 51; Mismatches 105; Indels 27; Gaps 7;
 QY 8 VKGLVAVITGASGLGATATARLVGGASAVLLDLPNSGGEAQAQK-----GN 56
 DB 9 LRSALAVTGGSGIGRAVSRLAGEGATVAACDLDRAAAGTETVRLGGPGSGKEGPPRN 68
 QY 57 NCVAPADVTSEKVOVALALAKGKGR-DVAVNVCAGIIVASKTYNLRKGGHTHLEDFQ 115
 DB 69 HAAP-QADVSEARARCLLEQVACFSRPSVYVSCAGITQDEFILHSE-----DDWD 121
 QY 116 RVLDVLMGTFNVIRLVAGENGQNEPDGGQGVITWTASVAAFEGVGQAAYSASKG1 175
 DB 122 KVIAVNKGITLVQAQAALVSN-----GGRGSIINISSIVGAVGVNGQTVNAASAGV 176

QY 176 VGMTELPARDLAPIGIRVWTAPGLGFPILLSPEKYSNPLASQVPPSRGDPAEAYH 235
 DB 177 IGITGNAPELRHGRHRCNSVLPGLFAPDMTQKQVYDKITTEMIPM-GHLGDEVDAD 235
 QY 236 LVQ-AIENPFNGEVRILDAIRN 259
 DB 236 VVAFLASEDSGXITGTSVEVTGLFW 261
 RESULT 10
 FABG_VIBCH STANDARD; PRT; 244 AA.
 AC Q9KH7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
 acyl carrier protein reductase).
 GN FABG OR VC2021.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EI for N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
 Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A.,
 Gill S.R., Nelson K.E., Read J.D., Tettelin H., Richardson D.,
 McDonald L., Vamathevan J., Bass S., Qin H., Dragoi I., Sellars P.,
 Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 Fraser C.M.;
 RA "DNA sequence of both chromosomes of the cholera pathogen *Vibrio*
 cholerae";
 RT Nature 406:477-483(2000).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 NAD(P)(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 (SDR) FAMILY.
 CC -----
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 CC -----
 DR EMBL: AE004276; AAF95169.1; ALT_INT.
 DR HSSP: P19992; 1HDC.
 DR TIGR: VC2021; 1HDC.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KM Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
 FT NP_BIND 10 34 NADP (BY SIMILARITY).
 FT ACT_SITE 151 151 BY SIMILARITY.
 SQ SEQUENCE 244 AA; 25566 MW; 9FB2E827BD7CC3CE CRC64;
 Query Match 25.3%; Score 330.5; DB 1; Length 244;
 Best Local Similarity 32.0%; Pred. No. 1.3e-18;
 Matches 82; Conservative 54; Mismatches 103; Indels 17; Gaps 5;
 QY 7 SVKGLVAVITGASGLGATATARLVGGASAVLLDLPNSGGEAQAQKGNCFAPADVT 66
 DB 2 NLEKVALVITGASRGKIAELERKARVIGTATSESGAQAISDYLDNGKGNALVNT 61
 QY 67 SEKDVTALALAKGKGRDVAVNVCAGIIVASKTYNLRKGGHTHLEDFQVLDVLMGTF 126

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DB      62 NPESIEAVIKAITBEFGVDILVNNAGITRNLNMRKE-----EEMSDIMETNLSIF 115
OY      127 NVILVAGEMGONEPDGGGQGVITINTASVAAFEGVQGAASAKSGIGVMTLPIARDL 186
DB      116 RLKRAVLFGMMKK-----RQGRITNGSVYGTGNAGQAVYAAKAGVIGFTKSMAREV 169
OY      187 APIGRVMTIAPGLFETPLLSPEKSNFLASQVPPPRGDAEFAHLVQALTEHP-- 244
DB      170 ASRGVYVTFVAPGLEITDMTKALNDEQRTATLQAPV-AGRLGDEPRLASAV-AFLASPEA 227
OY      245 -FLNGEVIRLDGAIRM 259
DB      228 AYITGETLHVNGVM 243

RESULT 11
DHB8_MOUSE STANDARD; PRT; 260 AA.
AC P50171; Q60959; Q60958; Q921W2;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Estradiol 17 beta-dehydrogenase 8 (EC 1.1.1.62) (17-beta-HSD 8) (17-
DE beta-hydroxysteroid dehydrogenase 8) (K6 protein) (K6-6).
GN HSD17B8 OR HKB6 OR H2-KB6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE: Kidney;
RX MEDLINE-93180832; PubMed-8441417;
RA Aziz N., Maxwell M.M., St Jacques B., Brenner B.M.;
RT "Downregulation of K6, a novel gene encoded within the major
RT histocompatibility complex, in murine polycystic kidney disease.";
RL Mol. Cell. Biol. 13:1847-1853(1993).
RN [2]
RP ERRATUM.
RA Aziz N., Maxwell M.M., St Jacques B., Brenner B.M.;
RL Mol. Cell. Biol. 13:6614-6614(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6;
RX MEDLINE-96027630; PubMed-7559658;
RA Maxwell M.M., Nearing J., Aziz N.;
RT "K6 gene. Sequence and organization and aberrant regulation in
RT murine polycystic kidney disease.";
RL J. Biol. Chem. 270:25219-25219(1995).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-129/SvJ;
RA Rowen L., Qin S., Madan A., Loretz C., James R., Dors M., Mix L.,
RA Hall J., Lasky S., Hood L.;
RT "Sequence of the mouse major histocompatibility locus class II
RT region.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: USES ESTRADIOL AS ITS PREFERRED SUBSTRATE.
CC -1- CATALYTIC ACTIVITY: Estradiol-17-beta + NAD(P)(+) = estrone +
CC NAD(P)H.
CC -1- PATHWAY: BIOSYNTHESIS OF ESTROGENS.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, A SHORT FORM (SHOWN HERE) AND A
CC LONG FORM, ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: KIDNEY, LIVER AND MODERATELY IN SPLEEN, HEART
CC AND BRAIN.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
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CC -----
DR EMBL; U34072; AAC53573.1; -
DR EMBL; U34072; AAC53574.1; -
DR EMBL; AF100956; AAC69902.1; -
DR HSSP; 070351; 1E6W.
DR MGD; MGI:95511; H2-K66.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PROSITE; PS00061; ADH_SHORT; 1.
KM Steroid biosynthesis; Oxidoreductase; NAD; Multigene family;
KM Alternative splicing
FT NP_BIND 13
FT ACT_SITE 168
FT VARSPIC 257
FT
FT CONFLICT 16
FT CONFLICT 17
FT CONFLICT 230
SQ SEQUENCE 260 AA; 26645 MW; 19C712FCDD158B08 CRC64;

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Query Match 24.3%; Score 316.5; DB 1; Length 260;
 Best Local Similarity 31.0%; Pred. No. 1,6e-17;
 Matches 85; Conservative 54; Mismatches 106; Indels 29; Gaps 9;

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OY 1 MAACRSVGLAVITGGA-SGLGATAEVLVGAGASAVLLDLPNSGPAQAKRLGN-- 56
DB 1 MASQLR-LRSALLAVYGGAGSGIGRILSVRLAEGAAVACDLGAAADYRLRILGSPS 59
OY 57 -----NCVFPADVTSEKDVQRLALAKGFGR-VDAVNCAGIAVASTYLNKKQ 107
DB 60 EDGAPRGRKNAF-QADVDSOGPAARRLLERVOACFSRPPVSVSCAGITDEFLHMS-- 116
OY 108 THRTLEDFORLDVNLGDTNVLVAGEMGONEPDGGGQGVITINTASVAAFEGVQGA 167
DB 117 -----EDMDRVIANVLGFTLVYQAAQALVSS-----GRRGSLINSSILGKVGNIQGN 167
OY 168 YSASKGIGVMTLPIARDLAPIGIRVMTIAPGLFETPLLSPEKSNFLASQVPPSR 227
DB 168 YASSKAGVIGITGTARELRGRIRGNSVLPGPFIATPMQKPEKVDKVTAMIPV-GHM 226
OY 228 GDPAEYAHLYQ--AIENPFLNGEVRRLDGAIRM 259
DB 227 GDPEDVADVAVFLASEDSGITGASVEVSGGLEFM 260

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RESULT 12
FABG_BACSU STANDARD; PRT; 246 AA.
AC P51831; Q31733;
DT 01-OCT-1986 (Rel. 34, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-oxoacyl-lacyl-carrier protein reductase (EC 1.1.1.100) (3-ketoacyl-
DE acyl carrier protein reductase).
GN FABG.
OS Bacillus subtilis.
CC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID:1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-168;
RX MEDLINE-96326321; PubMed-8759840;
RA Morbidoni H.R., de Mendoza D., Cronan J.E. Jr.;
RT "Bacillus subtilis acyl carrier protein is encoded in a cluster of
RT lipid biosynthesis genes.";
RL J. Bacteriol. 178:4794-4800(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-168;
RX MEDLINE-98044033; PubMed-9384377;

```


KW Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
 FT NP_BIND 11 NADP (BY SIMILARITY).
 ACT_SITE 156 BY SIMILARITY.
 SO SEQUENCE 247 AA; 25724 MM; 91EEF9409C777E20 CRC64;

Query Match 24.0%; Score 312.5; DB 1; Length 247;
 Best Local Similarity 32.1%; Pred. No. 3.1e-17;
 Matches 85; Conservative 45; Mismatches 92; Indels 43; Gaps 8;

QY 12 VAVITGGASGLGATAEPLVGGQ-----ASVLLDLPNSGGEAOKKLGNNC 58
 DB 8 VALVTGASRGIGATATLALANGMKVYVNTAOSSTADYVAEILANGSEA----- 58
 QY 59 VFAPADVTSEKDYOTALAKGKFGVDVAVNCAGIAVASKTYNLEKGGTHLEDFQRYL 118
 DB 59 IAVQAVNANADEVDOLIKETLDFSRIDVLVNNAGITRDITLLRMK-----LEDMQAVI 112
 QY 119 DVNLGMGFNYIRLVAGMGONEPDGOGGVIIINTSVAFEGVGOAAVSAKSGIGVM 178
 DB 113 DNLGVFLCTKAVSKIMLKQ-----KSGRIINTSVAGMGONPCQANYSAAKAGVIGF 166
 QY 179 TLEPIADLAFIGIRVMTIAPGLFETPLTSL-PEKYSNFLASQVPPSRGDPAEYAHLV 237
 DB 167 TKIVAKELASRGTVANAVAPGFATDMETENLNEPIIQF-----IPL-ARYGQEEVAGTI 221
 QY 238 QALIENP---FLNGEYIRLDGATRM 259
 DB 222 RFLATDPAALVITGQTFPNDGKVM 246

RESULT 14
 YK02_MYCTU STANDARD; PRT; 260 AA.
 AC Q10855;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Putative oxidoreductase RV2002 (EC 1.1.1.1).
 GN FARG3 OR RV2002 OR MT2058 OR MTCY39.16C.
 OS Mycobacterium tuberculosis.
 CC Bacteria; Actinobacteria; Actinobacteriia (class); Actinobacteridae;
 CC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 OC NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Broesch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeyer K., Gas S., Barry C.E. III, Tekala F.,
 RA Baddock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holtroyd S.,
 RA Hornsby T., Jagels K., Kirogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sultson J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., Deboy R., Dodson R., Gwyn M.L., Haft D., Hickey E.,
 RA Kojima J.F., Nelson W.C., Umayam L.A., Ermolova M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Kouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -i- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDOXTASES
 CC (SDR) FAMILY.
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DR EMBL: 274025; CA98414.1;
 DR EMBL: AE007057; AAK46335.1;
 DR HSSP: P19992; IHDC.
 DR TIGR: MT2058;
 DR TubercuList: RV2002;
 DR InterPro: IPR002198; ADL_short.
 DR Pfam: PF00106; adl_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADL_SHORT; 1.
 KW Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
 FT NP_BIND 11 35 NAD (BY SIMILARITY).
 FT ACT_SITE 153 153 BY SIMILARITY.
 FT CONFLICT 174 174 S -> G (IN REF. 2).
 FT SEQUENCE 260 AA; 27030 MM; 0935A14ED36220B7 CRC64;

Query Match 23.4%; Score 305; DB 1; Length 260;
 Best Local Similarity 33.9%; Pred. No. 1.2e-16;
 Matches 85; Conservative 41; Mismatches 99; Indels 26; Gaps 5;

QY 10 GIVAVITGGASGLGATAEPLVGGQASAVLLDLPNSGGEAOKKLGNNCFAPADVTSEK 69
 DB 7 GRVALVSGGARGMGSHVRANVABGAKVYFDIIDEBSKAAVAELADARVHLDYQPA 66
 QY 70 DVOTALALAKGKFGVDVAVNCAGIAVASKTYNLEKGGTHLEDFQRYLVNMGTEVYI 129
 DB 67 QMTAAVDAVTAFTAGLHLVNNAGI-----LNTGIDYALTQORILDNLTGVFLGI 120
 QY 130 RLVAGMGONEPDGOGGVIIINTSVAFEGVGOAAVSAKSGIGVMTPIRADAPI 189
 DB 121 RAVV-----KMKRAGRSITINISIGLAGYVACHGYITKRAVRGILITALEGPS 174
 QY 190 GIVATVAPGLFETPLTSLPEKYSNFLASQVPPSRG---DPAEYAHLV-QALIENP 244
 DB 175 GIRVNSIHGVLKVTMTWVPEDI-----FQTALGRAAEVPEVSNLVVYLSDESS 225
 QY 245 FLNGEYIRLDG 255
 DB 226 YSTGAEFVVDG 236

RESULT 15
 YWFD_BACSU STANDARD; PRT; 255 AA.
 AC P39640;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical oxidoreductase ywfd (EC 1.1.1.1).
 GN YWFD OR IPA-82D.
 OS Bacillus subtilis.
 CC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
 OC NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=95020537; PubMed=7934828;
 RA Glaser P., Kunst F., Arnaud M., Coucard M.P., Gonzales W.,
 RA Rillo M.F., Ionescu M., Lubochinsky B., Marcelino L., Mosser I.,
 RA Presecan E., Sautana M., Schneider E., Schweizer J., Vertes A.,
 RA Rapoport G., Danchin A.;
 RT "Bacillus subtilis genome project: cloning and sequencing of the 97
 RT kb region from 325 degrees to 333 degrees."
 RL M01. Microbiol. 10:371-384(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;

RA MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
RA Azavedo V., Bertero M.G., Bessieres P., Bolotin A., Borbett S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuno V., Carter N.M.,
RA Choi S.K., Codani J.J., Connetton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Erington J., Fabret C., Ferrari E., Fougere D.,
RA Fritz C., Fujita M., Goffeau A., Goldlighty E.J., Grandi G.,
RA Ghim S.Y., Glaser P., Goffeau A., Goldlighty E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Haelegh J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasehara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C.,
RA Medina N., Melado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,
RA Patro V., Pohl T.M., Portetelle D., Portwollik S., Prescott A.M.,
RA Priesean E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takeman K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Toseo V., Uchiyama S., Vandenbol M., Vannier P., Vassartoli A.,
RA Vitai A., Wanduit R., Wedler E., Wedler H., Wellzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*
RT *subtilis*".
RT Nature 390:249-256(1997).
RL Nature 390:249-256(1997).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
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CC or send an email to license@isb-sdb.ch).
CC
CC EMBL: X73124; CA51638.1;
CC EMBL: 299123; CA51579.1;
CC PIR: S39737; S39737.
CC HSP: P50162; IAE1.
CC Subtilisin; BG10628; ywfd.
CC InterPro: IPR002198; ADH_short.
CC Pfam: PF00106; adh_short.1.
CC PRINTS: PR00080; SDRFAMILY.
CC PROSITE: PS00061; ADH_SHORT.1.
KW Hypothetical protein; Oxidoreductase; Complete proteome.
FT NP_BIND 11 33 NAD OR NADP (BY SIMILARITY).
FT ACT_SITE 154 154 BY SIMILARITY.
SQ SEQUENCE 255 AA; 27324 MW; 20AA22595FB86C9B CRC64;

Query Match 23.3%; Score 304; DB 1; Length 255;
Best Local Similarity 31.7%; Pred. No. 1.5e-16;
Matches 86; Conservative 41; Mismatches 94; Indels 50; Gaps 7;

QY 14 VITGASGIGLATAERLVGQASAVLLDLPNSGCGAQAQKKGNNCV-FAPADVTSEKYO 72
D 11 ITTGASGIGYAAVAFPGQQAANVVADIIDEAGQAMKNNRLHFVQDITDEAQC 70
QY 73 TALALAKGFGVADVAVNCAGIAVASKTYNLKKGCTHLEDFORVLVDNLGTEFVAR-- 130
D 71 HAVESAVHFTFGDLVLINNAIGETIAPIHME-----LSDMNKVLQYNLNLGFMLSMHA 124
QY 131 ----LVAGEMGQNEPDQGGQGVITNTASVAAFEQGVQQAAYASASKGIVGKTLPIARDL 186
D 125 LKHMALAG-----KGNINTCSVSGIVAMPDIPAYNNAKSGVGLDITKSMADV 172

QY 187 APGIRKMTIAPLFGTPTL-----LTSLPKYSNFLASQVPPPSRLGDA 231
D 173 AKQIVNCVCPOEIDITPLNKSFLNNEGTLEIKKAKYKPNPL-----RKGPE 224
QY 232 EYAHVQAITE--NPLNGEVIRFLOCAIRMQ 260
D 225 EIANVNLFLASDLSSYMTGSAITADGQYTAQ 255
RESULT 16
2BHD_STREX STANDARD; PRT; 255 AA.
ID 2BHD_STREX
AC P19992;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE 20-beta-hydroxysteroid dehydrogenase (EC 1.1.1.53).
OS Streptomyces exfoliatus (Streptomyces hydropneumans).
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1905;
RN [1]
RP MEDLINE=90306362; PubMed=2194840;
RX MEDLINE=92052211; PubMed=1946424;
RA Ghosh D., Weeks C.M., Grochowski P., Duax W.L., Erman M.,
RA Rimsay R.L., Orr J.C.;
RT "Three-dimensional structure of holo 3 alpha,20 beta-hydroxysteroid
RT dehydrogenase: a member of a short-chain dehydrogenase family".
RL Proc. Natl. Acad. Sci. U.S.A. 88:10064-10068(1991).
CC -1- CATALYTIC ACTIVITY: Androstane-3-alpha,17-beta-diol + NAD(+) -> 17-
CC beta-hydroxyandrostane-3-one + NADH.
CC
CC -1- SUBUNIT: HOMOTETRAMER.
CC
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC PIR: S10707; S10707.
DR PDB: 2HSD; 31-AUG-94.
DR PDB: 1HDC; 07-FEB-95.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT.1.
KW Oxidoreductase; NAD; Steroid metabolism; 3D-structure.
FT NP_BIND 10 34 NAD (BY SIMILARITY).
FT ACT_SITE 152 152
SQ SEQUENCE 255 AA; 26484 MW; 9CB93CB66AA628D5 CRC64;

Query Match 23.2%; Score 302; DB 1; Length 255;
Best Local Similarity 33.6%; Pred. No. 2.1e-16;
Matches 85; Conservative 47; Mismatches 101; Indels 20; Gaps 8;

QY 8 VKGIVAVITGASGIGLATAERLVGQASAVLLDLPNSGCGAQAQKKGNNCV-FAPADVYS 67
D 4 LSGTAVITGASGIGLATAERLVGQASAVLLDLPNSGCGAQAQKKGNNCV-FAPADVYS 63
QY 68 EKVDTALALAKGFGVADVAVNCAGIAVASKTYNLKKGCTHLEDFORVLVDNLGTEFVAR-- 127
D 64 EEDQRYAAVAAAREFGVADVAVNCAGIAVASKTYNLKKGCTHLEDFORVLVDNLGTEFVAR-- 117
QY 128 VIRLVAGEMGQNEPDQGGQGVITNTASVAAFEQGVQQAAYASASKGIVGKTLPIARDL 187
D 118 GMRKIVIRAM-----KDAG--GSIYNTSSAGMLGIALTSSYGSKMGVRLSKLAAYELG 171
QY 188 PIGIRVKTAPGLFGLPL--TSLPKYSNFLASQVPPPSRLG-DPAEYAHVQAITE-- 242
D 172 TDRIRVNSVHPGKMTYTPMETGIRGEGNY--PMPFM--GRVGNRGEIAGAVVKKLSDT 228

QY 243 NPFLNGEVIRLDG 255
Db 229 SSVYTGAEALVDG 241

RESULT 17

Y4VI_RHISN STANDARD; PRT; 548 AA.

DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Putative short-chain type dehydrogenase/reductase Y4VI (EC 1.-.-.-).
GN Y4VI.
OS Rhizobium sp. (strain NGR334).
CG Plasmid sym PNGR234.
CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OX Rhizobiaceae; Rhizobium.
RN NCBI_TaxID=394;
RP SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freiberg C.A., Fellay R., Balroch A., Broughton W.J., Rosenthal A.,
RT "Molecular basis of symbiosis between Rhizobium and legumes.";
RL Nature 387:394-401(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96389014; PubMed=8796346;
RA Freiberg C., Perret X., Broughton W.J., Rosenthal A.;
RT "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.
RT NGR334 using dye terminators and a thermostable 'sequenase': a
RT beginning.";
RL Genome Res. 6:590-600(1996).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY. CONTAINS TWO DOMAINS.

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CC or send an email to license@sib-sib.ch).

CC EMBL; Z68203; CAA92424.1; ALT_INTT.
DR EMBL; AE000101; AAB91897.1; -.
DR HSSP; P50163; 2AE1.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 2.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
KW Multifunctional enzyme.
FT DOMAIN 1 250
FT DOMAIN 271 548
FT NP_BIND 12 37 SHORT-CHAIN DEHYDROGENASE/REDUCTASE 1.
FT NP_BIND 154 154 NAD OR NADP (BY SIMILARITY).
FT ACT_SITE 280 304 BY SIMILARITY.
FT NP_BIND 304 304 NAD OR NADP (BY SIMILARITY).
FT ACT_SITE 420 420 BY SIMILARITY.
SQ SEQUENCE 548 AA; 57593 MW; 399598C5DF17C23F CRC64;

Query Match 22.7%; Score 296.5; DB 1; Length 548;
Best Local Similarity 33.6%; Pred. No. 1.3e-15;
Matches 86; Conservative 40; Mismatches 101; Indels 29; Gaps 8;

QY 10 GIVAYITGGASGLGATLAEKLVGASAVLDDLPNSGGEAOAKKGNVCVAPADYISEK 69
Db 9 GIVAYITGGAGGIGALVDIFPAANGDVVAVDLPDSVGIETLGGNLPHEGLILEVDVSKED 68
QY 70 DVQATLALAKGKFGFVAVVAVNCAGI-----AVASKTYNKKGQTHLEDFORVLDVNLKMT 125
Db 69 DVVALRALLERKFSRIEVLVYNNAGIGPTMAATAD-----ALDFQALAINLVGA 119

QY 126 ENVIVLVAGENGQNEPDGGRGVITNTASVAAPFEGVGOAAYSAKSGIVGMLPIARD 185
Db 120 YSVACETAKIM---KPG-----AAVNVASLAGLGNPKRSAYSAKSLSTKSLACR 171
QY 186 LAPIGIRVMTIAPLFGTPIILTSLEPKYSNF-----LASQVPPSRIGDPAPAYAMLVQ--A 239
Db 172 WASRGIRVTAAPAGVHRIPMVAEL-ERAGKLDVSAIRRRVPL-GRIAPDEIARAVRELA 229
QY 240 IIEPFLNGEVIRLDG 255
Db 230 SAQASYITGSTLVVDG 245

RESULT 18

FABG_VIBRA STANDARD; PRT; 244 AA.

DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
DE acyl carrier protein reductase).
GN FABG.
OS Vibrio harveyi.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=669;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96134997; PubMed=8550484;
RC STRAIN=B392;
RA Shen Z., Myers D.M.;
RT "Isolation of Vibrio harveyi acyl carrier protein and the fabg, acpP,
RT and fabf genes involved in fatty acid biosynthesis.";
RL J. Bacteriol. 178:571-573(1996).
CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
CC PATHWAY.

CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.

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DR EMBL; U39441; AAC43589.1; -.
DR HSSP; P19992; 1HDC.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PRO0080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Fatty acid biosynthesis; Oxidoreductase; NADP.
FT NP_BIND 10 34 NADP (BY SIMILARITY).
FT ACT_SITE 151 151 BY SIMILARITY.
SQ SEQUENCE 244 AA; 25519 MW; FC41A16558CDDAA CRC64;

Query Match 22.5%; Score 293.5; DB 1; Length 244;
Best Local Similarity 29.8%; Pred. No. 8.9e-16;
Matches 76; Conservative 51; Mismatches 113; Indels 15; Gaps 4;

QY 7 SVKGLAVITGGASGLGATLAEKLVGASAVLDDLPNSGGEAOAKKGNVCVAPADYIT 66
Db 2 NEEKIALVTVGASRGIRTAIAELLVERGAVITTAISEGAAALISYLGNGGLANLT 61
QY 67 SEKDVATLALAKGKFGFVAVVAVNCAGIAYASTYVKKGQTHLEDFORVLDVNLKMT 126
Db 62 DVESEIETLKTINDEGCAIDIIIVNNAGITFDNLLMKMD-----DENMDIINTNLPIY 115
QY 127 NVIRLVAGENGQNEPDGGRGVITNTASVAAPFEGVGOAAYSAKSGIVGMLPIARD 186


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Db      116 RSKAVYLRGMKK-----RAGRINVSIVGTWGNAGQNTNYAAAGVIGFTKMAREV 169
Qy      187 APGIRVMTIAPGFGTPLTSLPEKVSNFLASQVFPSPRLGDPAEYAHLY--QALIEMP 244
Db      170 ASRGVYVNTYAPGFIETDMTKALNDQRAATLSNPV-AGRLGDPREIASVYVLASPEAA 228
Qy      245 FLNGEVIRLDGAIIM 259
Db      229 YITGETLHVNGGMM 243

RESULT 19
FABG_AQUAE STANDARD: PRT: 248 AA.
ID FABG_AQUAE
AC 067610;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
DE acyl carrier protein reductase).
GN FABG OR A0_11/16.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
OC Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VE5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Jenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aulay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RA "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus".;
RT Nature 392:353-358(1998).
RL
CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
CC PATHWAY.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
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CC -----
CC EMBL: AE000752; AAC07575.1; .
CC DR HSSB; p50163; 2AE1.
CC DR InterPro: IPR002198; ADH_short.
CC DR Pfam: PF00106; adh_short; 1.
CC DR PRINTS: PR00080; SDRFAMILY.
CC DR PROSITE: PS00061; ADH_SHORT; 1.
CC KM Fatty acid biosynthesis; Oxidoreductase; NADP. Complete proteome.
CC FT NP_BIND 12 36 NADP (37 SIMILARITY).
CC FT ACT_SITE 157 157 BY SIMILARITY.
CC FT SEQUENCE 248 AA; 26867 MW; 5CFD9EB9AD83F2C5 CRC64;
SQ

Query Match 22.5%; Score 293.5; DB 1; Length 248;
Best Local Similarity 30.0%; Pred. No. 9e-16;
Matches 77; Conservative 50; Mismatches 109; Indels 21; Gaps 6;
Qy      8 VKGLVAVITGASGLTAERLVGOGASAVILIDPNSGGEGQAACKLN---NCVAPPA 63
Db      5 LOGKYSLVGSTRGIRAIARLAKSAGSVIITGSGERARAVAEIANKYGVKAGVEM 64
Qy      64 DVTSEKDVOTALALAKGKFGKRVDAVNCAGIVASKTYNLKKGQHTLEDQRYVDNIM 123
Db      65 NLISESIVKAFEEIYLVGDIDILVNNAGITRDLFLRM-----SLIDEEVYLVNLT 118

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Qy      124 GTFNVIRLVAGEMGONEPDQGOR-GVITNPASVAAPFEGVQQAASKSGIVGMLPI 182
Db      119 GTFVLVONSRLRMK-----QRMGRVNISSVVGFTGNQGVNSTKAGLIGFTKSL 171
Qy      183 ARDLAPIGIRVMTIAPGFGTPLTSLPEKVSNFLASQVFPSPRLGDPAEYAHLYQALIE 242
Db      172 AKELAPRNVLVNAPGFIETDMTAVLSSEIIOXKKEQPLP-GRFGSEEVYANVYLFCS 230
Qy      243 N--PFLNGEVIRLDGAI 257
Db      231 ELASVITGEVHVNGGM 247

RESULT 20
FABG_ECOLI STANDARD: PRT: 244 AA.
ID FABG_ECOLI
AC P25716; P78821;
DT 01-NOV-1992 (Rel. 22, Created)
DT 01-NOV-1992 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
DE acyl carrier protein reductase).
GN FABG OR B1093.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=K12;
RX MEDLINE=92210530; PubMed=1556094;
RA Rawlings M., Cronan J.E. Jr.;
RA "The gene encoding Escherichia coli acyl carrier protein lies within
RT a cluster of fatty acid biosynthetic genes".;
RT J. Biol. Chem. 267:5751-5754(1992).
RL
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=97426517; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RA "The complete genome sequence of Escherichia coli K-12".;
RT Science 277:1234-1238(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Ostling T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Iiyemoto K., Inada T., Itoh T., Kajihara M., Kani K., Kasimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiiuchi T.;
RA "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map".;
RL DNA Res. 3:137-155(1996).
CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
CC PATHWAY.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
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CC -----
 DR EMBL: M84991; AAA23739.1; -
 DR EMBL: AE000210; AAC74177.1; -
 DR EMBL: D90745; BAA35901.1; -
 DR PIR: B42147; B42147.
 DR HSSP: P29132; 1DPI.
 DR Ecogene: EGI1318; fabg.
 DR Interpro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PRO0080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
 NP_BIND 10 34 NADP (BY SIMILARITY).
 FT ACT_SITE 151 151 BY SIMILARITY.
 FT CONFLICT 30 30 A->G (IN REF. 1).
 FT SEQUENCE 244 AA; 25560 MW; 48EC1F2AF7E9D9 CRC64;

Query Match 22.4%; Score 291.5; DB 1; Length 244;
 Best Local Similarity 30.0%; Pred. No. 1,3e-15;
 Matches 76; Conservative 50; Mismatches 112; Indels 15; Gaps 4;

QY 9 KGLVAVITGGASGSIATFARLVGOGASAVLLDLPNSGGEAOKLGNCFVAPADYTS 68
 DB 4 EGRITLVGASRGIGRAIAETLARGAKVISTATSENGAQLISDYLGANGKGLMNTDP 63
 QY 69 KDVOITALALARKGFRVDVAVNCAGIAVASKTYNLKKGQHTLEDFOQVLDVLMCTFN 128
 DB 64 ASIESVLEKIRAEGEVDILVNNAGITRDNLIMKMD-----EEMNDIETNLSYERL 117
 QY 129 IRLVAGEGONEPPOGGRGVITNTASAEQVGGAAYASAGSIVGVTLPRLAP 188
 DB 118 SKAVRAMMKR-----RGRITIGSVGVGGQANRAAGLIGFSKSLAREVAS 171
 QY 189 IGRVMTAPGLFETPLTSLPEKVSNFLASQVPEPSPRLGDPATYAHVQ-ATLENPTL 246
 DB 172 RGITVNVVAPGFIEDMTALSDQRAIGIQAQV-AGRLGAGCEIANVAVFLADENAYI 230
 QY 247 NGEVIRLDGAIRM 259
 DB 231 TGETLVHNGMYM 243

RESULT 21

BA71_EUBSP STANDARD; PRT; 249 AA.
 ID BA71_EUBSP
 AC P07914; 01-AUG-1988 (Rel. 08, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 7-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.159) (Bile acid
 7-dehydroxylase) (7-alpha-HSDH) (Bile acid-inducible protein).
 GN BAI1 AND BAI3.
 OS Eubacterium sp. (strain VPI 12708).
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=29347;
 RN [1]
 RP SEQUENCE FROM N.A. (BAI3).
 RX MEDLINE=90330548; PubMed=2376563;
 RA Gopal-Srivastava R., Mallonee D.H., White W.B., Hylemon P.B.;
 RT "Multiple copies of a bile acid-inducible gene in Eubacterium sp.
 strain VPI 12708.";
 RL J. Bacteriol. 172:4420-4426 (1990).
 RN [2]
 RP SEQUENCE FROM N.A. (BAI1).
 RX MEDLINE=86197993; PubMed=2834320;
 RA Coleman J.P., White W.B., Lifewski M., Hylemon P.B.;
 RT "Nucleotide sequence and regulation of a gene involved in bile acid
 7-dehydroxylation by Eubacterium sp. strain VPI 12708.";
 RL J. Bacteriol. 170:2070-2077 (1988).
 RN [3]
 RP SEQUENCE OF 1-55 FROM N.A. (BAI1), AND SEQUENCE OF 1-33.
 RX MEDLINE=87165759; PubMed=3549693;

RA Coleman J.P., White W.B., Hylemon P.B.;
 RT "Molecular cloning of bile acid 7-dehydroxylase from Eubacterium sp.
 strain VPI 12708.";
 RL J. Bacteriol. 169:1516-1521 (1987).
 CC -1- FUNCTION: 7-ALPHA-DEHYDROXYLATION OF CHOLIC ACID, YIELDING
 CC DEOXYCHOLIC ACID AND LITHOCHOLIC ACID, RESPECTIVELY. HIGHEST
 CC AFFINITY WITH TAUROCHENODEOXYCHOLIC ACID.
 CC -1- CATALYTIC ACTIVITY: 3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-
 CC cholanoate + NAD(+) = 3-alpha,12-alpha-dihydroxy-7-oxo-5-beta-
 CC cholanoate + NADH.
 CC -1- PATHWAY: Bile acid catabolism.
 CC -1- INDUCTION: PRESENCE OF C(24) BILE ACIDS CONTAINING A
 CC 7-ALPHA-HYDROXY GROUP.
 CC -1- SIMILARITY: THERE ARE THREE GENES FOR BAI1 PROTEINS: BAI1 IS
 CC IDENTICAL TO BAI3 AND THERE IS 81% IDENTITY WITH BAI2.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.

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 CC or send an email to license@sdb-sdb.ch).

CC EMBL: M34659; AAB61155.1; -
 CC EMBL: M19654; AAB61154.1; -
 CC EMBL: M15813; AAB61153.1; -
 DR PIR: A28212; A28212.
 DR PIR: A26938; A26938.
 DR PIR: B37762; B37762.
 DR HSSP: P19992; 1HDC.
 DR Interpro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PRO0080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Oxidoreductase; NAD; Bile acid catabolism; Multigene family.
 FT NP_BIND 7 13 NAD (POTENTIAL).
 FT NP_BIND 32 36 NAD (POTENTIAL).
 FT ACT_SITE 157 157 BY SIMILARITY.
 FT CONFLICT 159 162 TSKA -> YOGG (IN REF. 2).
 FT SEQUENCE 249 AA; 26658 MW; 084E380921D72C93 CRC64;

Query Match 22.3%; Score 291; DB 1; Length 249;
 Best Local Similarity 30.7%; Pred. No. 1.4e-15;
 Matches 83; Conservative 45; Mismatches 98; Indels 44; Gaps 10;

QY 8 VKGLVAVITGGASGLATFARLVGOGASAVLLDLPNSGGE-----AQAKR----- 53
 DB 4 VQKRIITIGTGTFIIFFAAKLEIENGAKYSIR-----GEOEVEDTALADIKLEYPER 57
 QY 54 --TGNCCVFPADVTSEKDVQFTALAKKKEGVVDVAVNCAGIAVASKTYNLKKGQHTL 111
 DB 58 EVLG---FAP-DLTSBDAAVAVGVAQYGRLDVNNAGITNMSVSRSE----- 106
 QY 112 EDFQVLDVNMGTFFVIRLVAGEGONEPPOGGRGVITNTASVAEFGVGAAYAS 171
 DB 107 EDFKINIDINVGVN-----GAMSAYCQMKDAKGVILNTASVIGISGLGTPRS 160
 QY 172 KGVIGVHTLPDIADLPICIRVNTAPGLFPLTSLPEKVSNFLASQVPEPSPRLG 231
 DB 161 KAAVYIGTGLGRELIRKIRIVVAVGVVDVTDMTGRLPEIUEDYLTLPV-KRLAKE 219
 QY 232 EYAHVQALITENPFLNG---EVIRLDGAIR 258
 DB 220 EIAN-VTLFLASDLASGITATITISVGAVR 248
 RESULT 22
 UCPA_SALTY STANDARD; PRT; 263 AA.
 ID UCPA_SALTY
 AC P37441;

DT 01-OCT-1994 (Rel. 30, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Oxidoreductase ucpa (EC 1.1.1.177).
 DE UCPA OR STM2445 OR STM2682.
 OS Salmonella typhimurium, and
 OC Salmonella typhi.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC NCBI_Taxid=602, 601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21534948; PubMed=11677609; / SGC1412 / ATCC 700720;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
 LT2".
 RL Nature 413:852-856(2001).
 RN [2]
 RP SEQUENCE OF 204-263 FROM N.A.
 RC SPECIES=S.typhimurium;
 RX MEDLINE=91358382; PubMed=1909324;
 RA Hryniewicz M.M., Kredich N.M.;
 RT "The cysP promoter of *Salmonella typhimurium*: characterization of two
 RT binding sites for CysB protein, studies of in vivo transcription
 RT initiation, and demonstration of the anti-inducer effects of
 RT thiosulfate".
 RL J. Bacteriol. 173:5876-5886(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.typhi; STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Kettlewell T., Hamlin N., Hargrett-Neale S., Jorgensen S.,
 RA Krogell M., Larsen T.S., Leather S., Mouton S., O'Garra P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrett B.G.;
 RT "Complete genome sequence of a multiple drug resistant *Salmonella*
 RT *enterica* serovar Typhi CT18".
 RL Nature 413:848-852(2001).
 CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
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 CC -----
 CC EMBL: AE008810; AAL21339.1; -;
 DR EMBL: AL627274; CAD07676.1; -;
 DR PIR: A38121; A38121.
 DR styGene: SGI0424; ucpa.
 DR InterPro: IPR002198; ADH_short.
 DR ProSite: PS00061; ADH_SHORT; FALSE_NEG.
 DR Oxidoreductase; Complete proteome.
 KW OXIDOREDUCTASE; COMPLETE PROTEOME.
 FT CONFLICT 218 L -> M (IN REF. 2).
 FT CONFLICT 258 S -> T (IN REF. 2).
 FT CONFLICT 263 V -> I (IN REF. 2).
 SQ SEQUENCE 263 AA; 27870 MW; 81826CAD94D534E CRC64;

QY 10 GIVAVITGAGSLGIATARNERLVGOGASAVLDDPNSNGENAOAKTL-----GNNCYFAP 62
 DB 6 KRTALITGASOGIGGIGARVFAHGHANILILDISD-----EIKLADLGRGHICRAVK 60
 QY 63 ADVTSEKDVOTALALAKGKFGVDAVAVACAGIYASKTYNLKGGTHLLEDFORVLDVNL 122
 DB 61 ADVRFPAVQAAVAAKATEGRIDILVNNACVCRGNFLDMS-----EDRFDHIDINI 114
 QY 123 MGTENVIRLVAGENGQNPDDGGORGVIINTASVAA-PEGVGAAYASASGGIVGMLP 181
 DB 115 KGVAVVTRAVLPEMKIKRD-----GRIVMMSVYGDVADPGETAYLSKAAIVGLTKS 168
 QY 182 IARDLAPIGIRVMTIAPGLGFTPLTSL-----PEKVSNFLASQVFPFSPRLGDAPEY 233
 DB 169 LAVEYAGSIRVNAICPGVRRPMAESIARQSNPDPEISYLEMAKAIPL-RLADPLEV 227
 QY 234 AHLVQ-ALLENPFLNGEYIRLDG 255
 DB 228 GELAAFLASDESSYLTGTQNVIDG 251
 RESULT 23
 PHBB_ALCEU
 ID PHBB_ALCEU STANDARD; PRT; 246 AA.
 AC P14697;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acetoacetyl-CoA reductase (EC 1.1.1.36).
 GN PHBB
 OS Alcaligenes eutrophus (Ralstonia eutropha).
 OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
 OC Ralstonia.
 RX NCBI_Taxid=510;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H16 / DSM 428 / ATCC 17699;
 RX MEDLINE=89359356; PubMed=2670935;
 RA Peoples O.P., Sinskey A.J.;
 RT "Poly-beta-hydroxybutyrate biosynthesis in *Alcaligenes eutrophus* H16.
 RT Characterization of the genes encoding beta-ketothiolase and
 RT acetoacetyl-CoA reductase".
 RL J. Biol. Chem. 264:15293-15297(1989).
 CC -1- CATALYTIC ACTIVITY: (R)-3-hydroxyacyl-CoA + NADP(+) -> 3-oxoacyl-CoA + NADPH.
 CC -1- PATHWAY: Poly-beta-hydroxybutyrate biosynthesis; second step.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
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 CC -----
 CC EMBL: J04987; AAA21973.1; -;
 DR PIR: B34340; RDAALAE.
 DR HSP: O70351; 1E3S.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAM1.
 DR ProSite: PS00061; ADH_SHORT; 1.
 KW Oxidoreductase; NADP; PHB biosynthesis.
 FT NP_BIND 8 NADP (BY SIMILARITY).
 FT ACT_SITE 153 BY SIMILARITY.
 SQ SEQUENCE 246 AA; 26370 MW; AD6739E0F593C06 CRC64;

Query Match 22.0%; Score 287; DB 1; Length 263;
 Best Local Similarity 32.2%; Pred. No. 3, 1e-15;
 Matches 85; Conservative 38; Mismatches 105; Indels 36; Gaps 8;

RT "Molecular and phylogenetic characterization of pyruvate and 2-
RT ketoglutarate ferredoxin oxidoreductases from *Pyrococcus furiosus*
RT and pyruvate ferredoxin oxidoreductase from *Thermotoga maritima*.";
RL J. Bacteriol. 178:248-257(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-MSB8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.W., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of *Thermotoga maritima*.";
CC Nature 399:323-329(1999).
CC -I- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
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CC -----
CC
DR EMBL: X85171; CA59459.1; -;
DR EMBL: AE001690; AAD35113.1; -;
DR HSSP: O70351; 1E6W.
DR TIGR: TM0019; -;
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Hypothetical protein; Oxidoreductase; NADP; Complete proteome.
FT NP_BIND 9 33 NADP (BY SIMILARITY).
FT ACT_SITE 153 153 BY SIMILARITY.
FT CONFLICT 130 136 RGGVIT -> TRWRSDH (IN REF. 1).
SQ SEQUENCE 256 AA; 28078 MW; D68160BD7980C6B CRC64;

Query Match 21.9%; Score 285.5; DB 1; Length 256;
Best Local Similarity 31.7%; Pred. No. 3.9e-15;
Matches 83; Conservative 45; Mismatches 113; Indels 21; Gaps 7;

QY 8 VKGLVAVITGGASGLATAEELVVGOGASAVLLDLPNSGG--EAQAKKLGNVCVFPAD 64
DB 2 LEKVAAYVTGGGGGGAIAQDLPAENGKMYIAIEDERAGVEREMLRKGLDVTFFKTD 61
QY 65 VTSEKDVOTALAKGKFRVDVAVNCAGIYVASKTYNLKKGQTHLEDFOVLDVNLNG 124
DB 62 VADENSVKNMYKRTVEIIGVDVLYNNAVMSKSIFF-----RPLEEMERYIRVNLTG 115
QY 125 TENVIRLVAGEMGOWEPGOGGORGIIINTASVAAFEQGVGOAAYSASKSGIVGMLPIAR 184
DB 116 PYICRYCAEMIK-----RGG--GYIINIASTRAFOSPEPTDEPYSASKGLVALTHSLAV 169
QY 185 DIAPIGIRVMTIAPGLFGRP--LITSLEPKVSNFLASGVPPPS--RLGDPAYAHLYQAI 241
DB 170 SLSRHYHIVSISPSWITSEMKSLRKKPDLRPIDHCHPAGRGVGNPLDIAMLCVPLA 229
QY 242 EMP---FLNGEVIRLDGAIRMO 260
DB 230 DDEKAGFTTGTNTFTVGGATVK 251

Thu Jun 26 06:55:06 2003

us-09-931-186-23.rapb

Page 1

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: June 23, 2003, 14:32:58 ; Search time 20.3333 Seconds
(without alignments)
1388.950 Million cell updates/sec

Title: US-09-931-186-23
Perfect score: 1304
Sequence: 1 MAACRSVKLVAVITGGAS.....ENPLUNGIVIRLDGATRMQP 261

Scoring table:
BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :
1: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubppaa/PCF_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubppaa/PCFUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1304	100.0	261	10	US-09-931-186-23 Sequence 23, Appl
2	1301	99.8	261	10	US-09-931-186-20 Sequence 20, Appl
3	1299	99.6	261	10	US-09-931-186-2 Sequence 2, Appl
4	1299	99.6	261	10	US-09-931-186-8 Sequence 8, Appl
5	1289	98.8	261	10	US-09-931-186-4 Sequence 4, Appl
6	1289	98.8	261	10	US-09-931-186-6 Sequence 6, Appl
7	1136	87.1	227	9	US-09-984-245-245 Sequence 245, App
8	1136	87.1	227	9	US-09-966-262-245 Sequence 245, App
9	1136	87.1	227	9	US-09-983-966-245 Sequence 245, App
10	1136	87.1	227	9	US-10-143-090-245 Sequence 245, App
11	667.5	51.2	388	9	US-09-920-923-41 Sequence 41, Appl
12	331.5	25.4	259	10	US-09-931-186-17 Sequence 17, Appl
13	329.5	25.3	243	10	US-09-815-242-13360 Sequence 1360, A
14	329.5	25.3	243	10	US-09-815-242-13581 Sequence 13581, A
15	321.5	24.7	245	10	US-09-815-242-10921 Sequence 10921, A
16	314	24.1	237	9	US-10-175-696-14 Sequence 14, Appl
17	314	24.1	237	9	US-09-823-901-2 Sequence 2, Appl
18	308.5	23.7	253	10	US-09-931-186-15 Sequence 15, Appl
19	302	23.7	247	8	US-09-478-040-9 Sequence 9, Appl
20	294.5	22.6	267	9	US-09-773-748-1 Sequence 1, Appl
21	293.5	22.5	262	9	US-10-307-385-6 Sequence 6, Appl
22	293.5	22.5	262	9	US-09-802-893-6 Sequence 6, Appl
23	291.5	22.4	244	10	US-09-815-242-10126 Sequence 10126, A
24	290.5	22.3	270	9	US-09-978-295A-468 Sequence 468, App
25	290.5	22.3	270	9	US-09-978-697-468 Sequence 468, App
26	290.5	22.3	270	9	US-09-978-192A-468 Sequence 468, App
27	290.5	22.3	270	9	US-09-999-832A-468 Sequence 468, App
28	290.5	22.3	270	9	US-09-978-188-468 Sequence 468, App
29	290.5	22.3	270	9	US-09-978-608A-468 Sequence 468, App
30	290.5	22.3	270	9	US-09-978-191A-468 Sequence 468, App
31	290.5	22.3	270	9	US-09-978-403A-468 Sequence 468, App
32	290.5	22.3	270	9	US-09-978-564A-468 Sequence 468, App
33	290.5	22.3	270	9	US-09-978-585A-468 Sequence 468, App
34	290.5	22.3	270	9	US-10-017-081A-468 Sequence 468, App
35	290.5	22.3	270	9	US-09-978-824-468 Sequence 468, App
36	290.5	22.3	270	9	US-09-981-915A-468 Sequence 468, App
37	290.5	22.3	270	9	US-09-999-833A-468 Sequence 468, App
38	290.5	22.3	270	9	US-10-167-749-468 Sequence 468, App
39	290.5	22.3	270	9	US-09-918-585A-468 Sequence 468, App
40	290.5	22.3	270	9	US-09-978-423A-468 Sequence 468, App
41	290.5	22.3	270	9	US-10-013-921A-468 Sequence 468, App
42	290.5	22.3	270	9	US-09-978-193A-468 Sequence 468, App
43	290.5	22.3	270	9	US-10-013-922A-468 Sequence 468, App
44	290.5	22.3	270	9	US-10-016-177A-468 Sequence 468, App
45	290.5	22.3	270	9	US-09-999-830A-468 Sequence 468, App
46	290.5	22.3	270	9	US-09-978-757A-468 Sequence 468, App
47	290.5	22.3	270	9	US-09-978-187B-468 Sequence 468, App
48	290.5	22.3	270	9	US-09-978-643A-468 Sequence 468, App
49	290.5	22.3	270	9	US-10-166-709A-468 Sequence 468, App
50	287.5	22.0	244	9	US-09-849-092-13 Sequence 13, Appl
51	287.5	22.0	263	10	US-09-815-242-14092 Sequence 14092, A
52	286.5	22.0	246	9	US-09-964-847-6 Sequence 6, Appl
53	286.5	22.0	64.1	9	US-09-964-847-10 Sequence 10, Appl
54	286.5	22.0	64.1	9	US-09-964-847-19 Sequence 19, Appl
55	286.5	22.0	64.2	9	US-09-964-847-59 Sequence 59, Appl
56	286.5	22.0	64.2	9	US-09-964-847-61 Sequence 61, Appl
57	283.5	21.7	203	9	US-10-175-696-19 Sequence 19, Appl
58	283.5	21.7	203	10	US-09-823-901-7 Sequence 7, Appl
59	281	21.5	258	9	US-09-738-626-6436 Sequence 6436, Ap
60	275.5	21.1	222	10	US-09-815-242-14688 Sequence 12688, A
61	275	21.1	251	10	US-09-815-242-10241 Sequence 10241, A
62	274.5	21.1	285	10	US-09-815-242-55889 Sequence 5589, Ap
63	274	21.0	206	9	US-09-997-816-4 Sequence 2, Appl
64	273.5	21.0	254	9	US-09-978-858-2 Sequence 2, Appl
65	273.5	21.0	286	10	US-09-815-242-11860 Sequence 11860, A
66	272.5	20.9	246	10	US-09-815-242-3461 Sequence 5461, Ap
67	272.5	20.9	246	10	US-09-815-242-12123 Sequence 12123, A
68	272.5	20.9	246	10	US-09-815-242-12803 Sequence 12803, A
69	272.5	20.9	246	10	US-09-815-242-13100 Sequence 13100, A
70	269.5	20.7	252	10	US-09-815-242-10974 Sequence 10974, A
71	269	20.6	256	10	US-09-954-314-14 Sequence 14, Appl
72	268	20.6	251	9	US-10-272-419-20 Sequence 20, Appl
73	267	20.5	276	9	US-09-944-160-24 Sequence 24, Appl
74	265.5	20.4	252	9	US-09-910-033A-2 Sequence 2, Appl
75	264.5	20.3	258	9	US-10-156-055A-1 Sequence 1, Appl
76	260	19.9	253	10	US-09-815-242-11842 Sequence 11842, A
77	258	19.8	261	10	US-09-971-536-74 Sequence 74, Appl
78	255	19.6	261	10	US-09-940-037A-29 Sequence 29, Appl
79	254.5	19.5	266	9	US-09-981-353-40 Sequence 40, Appl
80	254.5	19.5	266	9	US-09-885-303A-22 Sequence 22, Appl
81	254.5	19.5	266	9	US-10-205-483-176 Sequence 176, App
82	249.5	19.5	266	10	US-09-931-186-18 Sequence 18, Appl
83	249.5	19.5	266	10	US-09-815-242-10597 Sequence 10597, A
84	249.5	19.1	221	10	US-09-764-885-553 Sequence 553, App
85	249	19.1	221	10	US-09-815-242-10846 Sequence 10846, A
86	243	18.7	251	10	US-09-922-501-16 Sequence 16, Appl
87	243	18.6	255	10	US-09-931-186-14 Sequence 14, Appl
88	243	18.6	255	10	US-09-931-186-11 Sequence 11, Appl
89	240.5	18.4	274	9	US-09-924-314-12 Sequence 12, Appl
90	240	18.4	247	10	US-09-916-059-17 Sequence 17, Appl
91	238	18.3	271	10	US-09-815-242-11893 Sequence 11893, A
92	238	18.3	271	10	US-09-815-242-13579 Sequence 13579, A

93 235 18.0 311 9 US-09-738-626-3819 Sequence 3819, Ap
94 231 17.7 261 10 US-09-815-242-5813 Sequence 5813, Ap
95 228.5 17.5 247 10 US-09-815-242-11342 Sequence 11342, A
96 226 17.3 254 10 US-09-741-669-411 Sequence 411, App
97 225.5 17.3 247 10 US-09-815-242-11514 Sequence 11514, A
98 222.5 17.1 900 9 US-10-060-230-15 Sequence 15, Appl
99 222.5 17.1 900 9 US-10-060-230-17 Sequence 17, Appl
100 221.5 17.0 253 10 US-09-815-242-10279 Sequence 10279, A

ALIGNMENTS

RESULT 1
US-09-931-186-23
Sequence 23, Application US/09931186
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABBRO, MELWYN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPICZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C214S
US-09-931-186-23

Query Match 100.0%; Score 1304; DB 10; Length 261;
Best Local Similarity 100.0%; Pred. No. 5,3e-110;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAACRSYKGLVAVITGGASGLGATAEELVGGASAVLLDLPNSGGEAOKKIGNCVF 60
DB 1 MAACRSYKGLVAVITGGASGLGATAEELVGGASAVLLDLPNSGGEAOKKIGNCVF 60
QY 61 APADVTSEKDVOTATLAKGKFGKRDVAVNCAGIAVASKTYNLKKGOTHTLEDFQRLVDV 120
DB 61 APADVTSEKDVOTATLAKGKFGKRDVAVNCAGIAVASKTYNLKKGOTHTLEDFQRLVDV 120
QY 121 NMGTFFNVIRLVAGEMGNEDDGGGQGVIIINTASVAAFEGQGAASASKGGIVGNTL 180
DB 121 NMGTFFNVIRLVAGEMGNEDDGGGQGVIIINTASVAAFEGQGAASASKGGIVGNTL 180
QY 181 PIARDAPIGIRVMTIAPGLTGLTLLSLPEKVSNTFLASQVPPSRIGDDPAEYAHLYOAI 240
DB 181 PIARDAPIGIRVMTIAPGLTGLTLLSLPEKVSNTFLASQVPPSRIGDDPAEYAHLYOAI 240
QY 241 IENPFLNGEVIRLDGAIRMOP 261
DB 241 IENPFLNGEVIRLDGAIRMOP 261

RESULT 2

US-09-931-186-20
Sequence 20, Application US/09931186
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABBRO, MELWYN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPICZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C214A
US-09-931-186-20

Query Match 99.8%; Score 1301; DB 10; Length 261;
Best Local Similarity 99.6%; Pred. No. 9,9e-110;
Matches 260; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAACRSYKGLVAVITGGASGLGATAEELVGGASAVLLDLPNSGGEAOKKIGNCVF 60
DB 1 MAACRSYKGLVAVITGGASGLGATAEELVGGASAVLLDLPNSGGEAOKKIGNCVF 60
QY 61 APADVTSEKDVOTATLAKGKFGKRDVAVNCAGIAVASKTYNLKKGOTHTLEDFQRLVDV 120
DB 61 APADVTSEKDVOTATLAKGKFGKRDVAVNCAGIAVASKTYNLKKGOTHTLEDFQRLVDV 120
QY 121 NMGTFFNVIRLVAGEMGNEDDGGGQGVIIINTASVAAFEGQGAASASKGGIVGNTL 180
DB 121 NMGTFFNVIRLVAGEMGNEDDGGGQGVIIINTASVAAFEGQGAASASKGGIVGNTL 180
QY 181 PIARDAPIGIRVMTIAPGLTGLTLLSLPEKVSNTFLASQVPPSRIGDDPAEYAHLYOAI 240
DB 181 PIARDAPIGIRVMTIAPGLTGLTLLSLPEKVSNTFLASQVPPSRIGDDPAEYAHLYOAI 240
QY 241 IENPFLNGEVIRLDGAIRMOP 261
DB 241 IENPFLNGEVIRLDGAIRMOP 261

RESULT 3
US-09-931-186-2
Sequence 2, Application US/09931186
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABBRO, MELWYN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPICZYK-RUSSELL, ANNA

Page 3

Query Match	99.6%	Score 1299;	DB 10;	Length 261;
Best Local Similarity	99.6%	Pred. No. 1.5e-109;		
Matches 260; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

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241 IENPFLNGEVRIDGAI RMQP 261
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241 IENPFLNGEVRIDGAI RMQP 261
b      |||||

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SEQ ID NO 8
LENGTH: 261
TYPE: PRT
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Query Match	99.6%	Score 1299;	DB 10;	Length 261;
Best Local Similarity	99.6%	Pred. No. 1.5e-109;		
Matches 260; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

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y      241 IENPFLNGEVRLLDGAIRMQP 261
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b      241 IENPFLNGEVRLLDGAIRMQP 261

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FEATURE:
OTHER INFORMATION: full length mutant ERAB C5V
S-09-931-186-4

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61 APADVTSEKDVTALALANGKFGRYDVAVNCAGIAVASKTYNMLKKGQHTTLEDFQRLVDV 120

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Db 121 NLMGTFNVLVAGEMQNEPDGQGRVLIINTASVAAEQGVQCAAYSASKGIVGML 180
QY 181 PIARDLAPIGIRVWTIPGIFGPIPLTSLPEKYSNFIASQVPPPSRLGDAEYAHVQAI 240
Db 181 PIARDLAPIGIRVWTIPGIFGPIPLTSLPEKYSNFIASQVPPPSRLGDAEYAHVQAI 240
QY 241 IENPFLNGEVIIRLDGAIIRMP 261
Db 241 IENPFLNGEVIIRLDGAIIRMP 261
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RESULT 6
US-09-931-186-6
; Sequence 6, Application US/09931186
; Patent No. US20020132319A1
; GENERAL INFORMATION:
; APPLICANT: ABBRO, MELWYN A.
; APPLICANT: AUST, ROBERT
; APPLICANT: KISSINGER, CHARLES R.
; APPLICANT: MARGOSIAX, STEVE
; APPLICANT: MENG, JERRY J.
; APPLICANT: PELLETIER, LAURA A.
; APPLICANT: REJTO, PAUL A.
; APPLICANT: SHOWALTER, RICHARD E.
; APPLICANT: TEMPCZYK-RUSSELL, ANNA
; APPLICANT: THOMSON, JIM
; APPLICANT: VANDERPOOL, DARIN
; APPLICANT: VILLAFRANCA, J. ERNEST
; TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
; TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
; TITLE OF INVENTION: OF INHIBITORS THEREOF
; FILE REFERENCE: 0125-0049
; CURRENT APPLICATION NUMBER: US/09/931.186
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: full length mutant ERAB C58V
US-09-931-186-6
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Query Match 98.8%; Score 1289; DB 10; Length 261;
Best Local Similarity 99.2%; Pred. No. 1.2e-108;
Matches 259; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 1 MAACRSYKGLVAVITGGASGLGATAEKLVGASASVLLDLPNSGGEQAQKLGNNCVF 60
QY 61 APADVTSEKDVOTLALAKKFGKGVDAVAVNAGIAVASKTYNLLKKQTHLEDEQRYLDV 120
Db 61 APADVTSEKDVOTLALAKKFGKGVDAVAVNAGIAVASKTYNLLKKQTHLEDEQRYLDV 120
QY 121 NLMGTFNVLVAGEMQNEPDGQGRVLIINTASVAAEQGVQCAAYSASKGIVGML 180
Db 121 NLMGTFNVLVAGEMQNEPDGQGRVLIINTASVAAEQGVQCAAYSASKGIVGML 180
QY 181 PIARDLAPIGIRVWTIPGIFGPIPLTSLPEKYSNFIASQVPPPSRLGDAEYAHVQAI 240
Db 181 PIARDLAPIGIRVWTIPGIFGPIPLTSLPEKYSNFIASQVPPPSRLGDAEYAHVQAI 240
QY 241 IENPFLNGEVIIRLDGAIIRMP 261
Db 241 IENPFLNGEVIIRLDGAIIRMP 261
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RESULT 7
US-09-984-245-245
; Sequence 245, Application US/09984245
; Patent No. US20020165374A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/984,245
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 245
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-245-245
Query Match 87.1%; Score 1136; DB 9; Length 227;
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Page 5

Best Local Similarity 99.6%; Pred. No. 6,5e-95;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 95 AVASTYLNKKGGQHTLEDFQRYLDVNLMTGFENVIRLVAGEMQNEPDGQGRGVYIINTA 154
    |||||||
Db 61 AVASTYLNKKGGQHTLEDFQRYLDVNLMTGFENVIRLVAGEMQNEPDGQGRGVYIINTA 120
QY 155 SVAAFEGQVGAAYASASKSGIVGNTLPARDLAPIGIRVMTIAPGLFGPTLTSLEPKVS 214
    |||||||
Db 121 SVAAFEGQVGAAYASASKSGIVGNTLPARDLAPIGIRVMTIAPGLFGPTLTSLEPKVC 180
QY 215 NFLASQVFPSPRLGDPAPAYAHVQAIIENPFLNGEVIRLDGAIRMOP 261
    |||||||
Db 181 NFLASQVFPSPRLGDPAPAYAHVQAIIENPFLNGEVIRLDGAIRMOP 227
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RESULT 8
US-09-966-262-245

; Sequence 245, Application US/09966262
; Publication No. US20030050461A1

; GENERAL INFORMATION:

; APPLICANT: Young et al.

; TITLE OF INVENTION: 87 Human Secreted Proteins

; FILE REFERENCE: P2004P1

; CURRENT APPLICATION NUMBER: US/09/966,262

; PRIOR FILING DATE: 2001-10-01

; PRIOR APPLICATION NUMBER: US 09/154,707

; PRIOR FILING DATE: 1998-09-17

; PRIOR APPLICATION NUMBER: PCT/US98/05311

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: US 60/041,277

; PRIOR FILING DATE: 1997-03-21

; PRIOR APPLICATION NUMBER: US 60/042,344

; PRIOR FILING DATE: 1997-03-21

; PRIOR APPLICATION NUMBER: US 60/041,276

; PRIOR FILING DATE: 1997-03-21

; PRIOR APPLICATION NUMBER: US 60/041,281

; PRIOR FILING DATE: 1997-03-21

; PRIOR APPLICATION NUMBER: US 60/048,094

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,350

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,188

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,135

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/050,937

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,186

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,069

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,095

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,131

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,096

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,355

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,160

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,351

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; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 245
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-966-262-245
Query Match 87.1%; Score 1136; DB 9; Length 227;
Best Local Similarity 99.6%; Pred. No. 6,5e-95;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 35 ASAYLDLPNSGGEAQAQKLNCCVAPADVTSEKDVQTAALAKKFRGVAVNCAGI 94
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Db 1 ASAYLDLPNSGGEAQAQKLNCCVAPADVTSEKDVQTAALAKKFRGVAVNCAGI 60
QY 95 AVASTYLNKKGGQHTLEDFQRYLDVNLMTGFENVIRLVAGEMQNEPDGQGRGVYIINTA 154
    |||||||
Db 61 AVASTYLNKKGGQHTLEDFQRYLDVNLMTGFENVIRLVAGEMQNEPDGQGRGVYIINTA 120
QY 155 SVAAFEGQVGAAYASASKSGIVGNTLPARDLAPIGIRVMTIAPGLFGPTLTSLEPKVS 214
    |||||||
Db 121 SVAAFEGQVGAAYASASKSGIVGNTLPARDLAPIGIRVMTIAPGLFGPTLTSLEPKVC 180
QY 215 NFLASQVFPSPRLGDPAPAYAHVQAIIENPFLNGEVIRLDGAIRMOP 261
    |||||||
Db 181 NFLASQVFPSPRLGDPAPAYAHVQAIIENPFLNGEVIRLDGAIRMOP 227
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RESULT 9
US-09-983-966-245

; Sequence 245, Application US/09983966
; Publication No. US20030060619A1

; GENERAL INFORMATION:

; APPLICANT: Young et al.

; TITLE OF INVENTION: 87 Human Secreted Proteins

; FILE REFERENCE: P2004P1

; CURRENT APPLICATION NUMBER: US/09/983,966

; PRIOR FILING DATE: 2001-10-29

; PRIOR APPLICATION NUMBER: 09/154,707

; PRIOR FILING DATE: 1998-09-17

; PRIOR APPLICATION NUMBER: PCT/US98/05311

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: US 60/041,277

; PRIOR FILING DATE: 1997-03-21

; PRIOR APPLICATION NUMBER: US 60/042,344

; PRIOR FILING DATE: 1997-03-21

; PRIOR APPLICATION NUMBER: US 60/041,276

; PRIOR FILING DATE: 1997-03-21

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; PRIOR APPLICATION NUMBER: US 60/048,094

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; PRIOR APPLICATION NUMBER: US 60/048,350

; PRIOR FILING DATE: 1997-05-30

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; PRIOR APPLICATION NUMBER: US 60/048,135

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/050,937

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,187

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,099

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; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
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; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 245
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-983-966-245
Query Match      87.1%; Score 1136; DB 9; Length 227;
Best Local Similarity 99.6%; Pred. No. 6.5e-95;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

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QY      35 ASAVLLDLPNSGGGAQAKKIGNNCFAPADYTSKDVQYALALAKGKFGRYDAVNCAGI 94
      1 ASAVLLDLPNSGGGAQAKKIGNNCFAPADYTSKDVQYALALAKGKFGRYDAVNCAGI 60
DB      95 AVASKTYNLKKGQHTLEDFQRYLDVNLMTGFNVIIRLVAGMGONEPDGGGQRYIINTA 154
      61 AVASKTYNLKKGQHTLEDFQRYLDVNLMTGFNVIIRLVAGMGONEPDGGGQRYIINTA 120
QY      155 SVAAFEQGYGQAAYSASKSGIGVGMTLPARDLAPIGIRVMTIAPGLTGPILTSLEPKYS 214
      121 SVAAFEQGYGQAAYSASKSGIGVGMTLPARDLAPIGIRVMTIAPGLTGPILTSLEPKYS 180
DB      215 NFLASQVPPPSRLGDPAEYAHVQAIIENPFLNGEVRIRLDGAIKRMOP 261
      181 NFLASQVPPPSRLGDPAEYAHVQAIIENPFLNGEVRIRLDGAIKRMOP 227
```

```

RESULT 10
US-10-143-090-245
; Sequence 245, Application US/10143090
; Publication No. US20030069406a1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004Pl
; CURRENT APPLICATION NUMBER: US/10/143,090
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 245
; LENGTH: 227
; TYPE: PRT
```

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; ORGANISM: Homo sapiens
; US-10-143-090-245
Query Match      87.1%; Score 1136; DB 9; Length 227;
Best Local Similarity 99.6%; Pred. No. 6.5e-95;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

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QY      35 ASAVLLDLPNSGGGAQAKKIGNNCFAPADYTSKDVQYALALAKGKFGRYDAVNCAGI 94
      1 ASAVLLDLPNSGGGAQAKKIGNNCFAPADYTSKDVQYALALAKGKFGRYDAVNCAGI 60
DB      95 AVASKTYNLKKGQHTLEDFQRYLDVNLMTGFNVIIRLVAGMGONEPDGGGQRYIINTA 154
      61 AVASKTYNLKKGQHTLEDFQRYLDVNLMTGFNVIIRLVAGMGONEPDGGGQRYIINTA 120
QY      155 SVAAFEQGYGQAAYSASKSGIGVGMTLPARDLAPIGIRVMTIAPGLTGPILTSLEPKYS 214
      121 SVAAFEQGYGQAAYSASKSGIGVGMTLPARDLAPIGIRVMTIAPGLTGPILTSLEPKYS 180
DB      215 NFLASQVPPPSRLGDPAEYAHVQAIIENPFLNGEVRIRLDGAIKRMOP 261
      181 NFLASQVPPPSRLGDPAEYAHVQAIIENPFLNGEVRIRLDGAIKRMOP 227
```

```

RESULT 11
US-09-920-923-41
; Sequence 41, Application US/09920923
; Publication No. US20030022273A1
; GENERAL INFORMATION:
; APPLICANT: Pasamontes, Luis
; APPLICANT: Tsygankov, Yuri
; TITLE OF INVENTION: Improved Fermentative Carotenoid Production
; FILE REFERENCE: Improved Fermentative Carotenoid
; CURRENT APPLICATION NUMBER: US/09/920,923
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 08/980,832
; PRIOR FILING DATE: 1997-12-01
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 41
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Flavobacterium sp. R1534
; US-09-920-923-41
Query Match      51.2%; Score 667.5; DB 9; Length 388;
Best Local Similarity 55.5%; Pred. No. 2.6e-52;
Matches 141; Conservative 35; Mismatches 69; Indels 9; Gaps 3;
```

```
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABBRO, MELWYN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAR, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REUTO, PAUL A.
APPLICANT: SHOMALTER, RICHARD E.
APPLICANT: TEMPCEYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLARRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
FILE REFERENCE: 0125-0049
CURRENT FILING DATE: 2001-08-17
CURRENT APPLICATION NUMBER: US/09/931.186
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 259
TYPE: PRT
ORGANISM: Homo sapiens
US-09-931-186-17

Query Match      25.4%: Score 331.5; DB: 10; Length 259;
Best Local Similarity 31.2%; Pred. No. 3.2e-22;
Matches 83; Conservative 51; Mismatches 105; Indels 27; Gaps 7;

QY 8 VKGLAVITGASGLGATARIYVGOGASAVLIDLPSNGGAQAQKL-----GN 56
DB 7 LRSALAVITGASGLGATARIYVGOGASAVLIDLPSNGGAQAQKL-----GN 56
QY 57 NCVPAPADVISEKVOYALALAKGFEGR-VDAVAVNCAQIAVASKTYNLKKGQHTLEDFO 115
DB 67 HAAP-QADVSEARARACILEQVQACFSRPSVYVSCAGITQDEFLHMS-----DDWD 119
QY 116 RVLVNLMGTENVRIYVAGEGMEPOGGORGVITINTASVAFAEGOVGOAAYASASRGSI 175
DB 120 KVIAVNLKGTFLVYQAAQALVSN-----GCRSITINISVGVGVANGVQNTYASAGV 174
QY 176 VGMFLPIARDLPIGIRVMTIAPGLFGTPLTSLPEKVSNFLASQVFPSPRLGDPAEYAH 235
DB 175 IGLTQFARLEGRRGIRNSVLPFGFIATPMTQKVPKVKVDEKITEMIM-CHLGDPEDVAD 233
QY 236 LVQ--AIENPELNGEVRIDGAIIRM 259
DB 234 VVAFLASEDSGYITGTSYEVYGLFM 259

RESULT 13
US-09-815-242-13360
Sequence 13360, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT FILING DATE: 2001-03-21
CURRENT APPLICATION NUMBER: US/09/815.242
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/131.078
```

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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206.848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207.727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242.578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253.625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257.931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269.308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13360
LENGTH: 243
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-815-242-13360

Query Match      25.3%: Score 329.5; DB: 10; Length 243;
Best Local Similarity 35.1%; Pred. No. 4.5e-22;
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;

QY 15 ITGASGLGATARIYVGOGASAVLIDLPSNGGE-----AQAKIGNNCVPAPADVISE 68
DB 10 ITGSRGIGLAIHAKRAQAGANIVL-----NSRGAISEELAEFSNKGIVPLSGVSDF 65
QY 69 KDVTALALAKGFGVYDAVAVNCAQIAVASKTYNLKKGQHTLEDFOPLVDNLMGTENV 128
DB 66 ADKKRMIIDQAIALGSDVPLVNNAGI--TQDTLMKLM---TEADEKVLKYNLTGAFNM 119
QY 129 IRLVAGEMGNEBPDOGGORGVITINTASVAFAEGOVGOAAYASASRGSI 188
DB 120 TQSVL-----KMMARREGAITNMSVYGMGNICQANAYASKGLIFTSVAERVAS 173
QY 189 IGRVMTIAPGLFGTPLTSLPEKVSNFLASQVFPSPRLGDPAEYAHVQALIEENPFLNG 248
DB 174 RNRVAVVIRAPGMIESTMTAIIISDKIKKAVTLAQIPM-KERGOAEOVADLVFLAGODYILG 232
QY 249 EVIRIDGAIIRM 259
DB 233 QVTAIDGGLSM 243

RESULT 14
US-09-815-242-13381
Sequence 13381, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT FILING DATE: 2001-03-21
CURRENT APPLICATION NUMBER: US/09/815.242
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/131.078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206.848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207.727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242.578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253.625
```


TYPE: PRT
ORGANISM: Bacillus megaterium
US-09-479-040-9

Query Match 23.2%; Score 303; DB 9; Length 247;
Best Local Similarity 29.1%; Pred. No. 1.1e-19;
Matches 78; Conservative 59; Mismatches 93; Indels 38; Gaps 9;

QY 7 SVNGIVVITGASGIGLATAERLVQG-----ASAVLDLPNSGGEQAK 53
DB 3 TLGGKVAIVTGGSKGGAATRELASNGKAVAVNSSSESAAIVKEIKDNGER---- 58
QY 54 LGNNCFAPADVTSEKDVOTALALAKGFRGVDAVAVNCAGIAVASKTYLKK-GQHTTLE 112
DB 59 -----IAYQADVSYVDQAKHLIETKAATFGQDILVNNNGI---TRDRFKKIGE-----E 106
QY 113 DFORVLDVNLMTFNVIRLVAGMGONPDGQGRVYIINTASVAAFEGOVGAAYSASK 172
DB 107 DMKKVIDVNLHSYNTTSALTLESE---GGR---VINISSIIQAGFGQNTYSAK 160
QY 173 GGIVGMLPIARLAPIGIRVMTIAPGLGTPPLTSLPEKVSNFLASOVPPSRIGDPAE 232
DB 161 AGMLGFTKSLALDELARTGYVNAICPGFIETEMVAIPEDVRAKIYAKIP-TRRLGHAE 219
QY 233 YAH-LVOAITENPFLNGEVRIRLDGAIRM 259
DB 220 IARGVYLANDGAVITGOOLININGLYM 247

RESULT 20

US-09-773-748-1
Sequence 1, Application US/09773748
Publication No. US20020187537A1
GENERAL INFORMATION:
APPLICANT: Wada, Masaru
TITLE OF INVENTION: Levodione reductase gene and use thereof
FILE REFERENCE: Levodione reductase
CURRENT APPLICATION NUMBER: US/09/773,748
CURRENT FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: EP00101665.8
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 267
TYPE: PRT
ORGANISM: Corynebacterium aquaticum
US-09-773-748-1

Query Match 22.6%; Score 294.5; DB 9; Length 267;
Best Local Similarity 31.8%; Pred. No. 7.4e-19;
Matches 84; Conservative 46; Mismatches 97; Indels 37; Gaps 9;

QY 12 VAVTGGASGIGLATAERLVQGSANVLDLPNSGGEQAKKGNMCVAP-----ADVT 66
DB 15 VVLTGGSSGIGRTAVRLAAEGAKSLVDVSSSEGLASRAAVLETPADEVLTVDVADVS 74
QY 67 SEKDVOOTALAKRFGRVDAVAVNCAGIAVASKTYLKKQGTHTLEDFORVLDVNLMTGF 126
DB 75 DEAGVEAVYVATTRFRIDGFFNNAGIEBKQ-----NPESTTAEFDDVYSINLRGVF 129
QY 127 -----NVIRLVAGMGONPDGQGRVYIINTASVAAFEGOVGAAYSASKGIVGMLPI 182
DB 130 LGIEKYLKIMR-----EGGS---GMVVTASVAGIRGIGNSGVYAAAKHGVVGLTRMS 179
QY 183 ARDLAPIGIRVMTIAPGLGTPPLTSL-----PEKVS-NFLASOVPPSRIGDPAEY 233
DB 180 AVEGRGIRINALAPGAIWTPWENSMKOLDPENPKAAEELI---QVNSKRYGAEPI 237
QY 234 AHLVQAIEN--PFLNGEVRIRLDG 255
DB 238 AAAYAFLLSDSDASVYVATVVIDG 261

RESULT 21
US-10-307-385-6
Sequence 6, Application US/10307385
Publication No. US2003007797A1
GENERAL INFORMATION:
APPLICANT: SUGIYAMA, MASAKAZU
APPLICANT: TONOUCHI, NAORO
APPLICANT: SUZUKI, SHUNICHI
APPLICANT: YOKOZUKI, KENZO
TITLE OF INVENTION: XYLIOTOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THERE
FILE REFERENCE: 0010-1024-0
CURRENT APPLICATION NUMBER: US/10/307,385
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: US/09/363,189
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: JP10-216047
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 262
TYPE: PRT
ORGANISM: Gluconobacter oxydans
US-10-307-385-6

Query Match 22.5%; Score 293.5; DB 9; Length 262;
Best Local Similarity 31.6%; Pred. No. 8.9e-19;
Matches 86; Conservative 42; Mismatches 109; Indels 35; Gaps 7;

QY 6 RSVKGLVAVITGASGIGLATAERLVQGSASAVILDPNSG---GEAQAKKGNMCVAP 62
DB 3 KRFNKGVCLVYTGAGGNIGLATAERLVQGSASAVILDPNSG---GEAQAKKGNMCVAP 62
QY 63 ADVTSEKDVOTALALAKRFGRVDAVAVNCAGIAVASKTYLKKQGTHTLEDFORVLDVNL 122
DB 63 CVTSEEAIVTGVDSVVDGFKIDPLFNAGYGA-----FAPVDYPSDDFARVLTIVN 117
QY 123 MGFNVIRLVAGMGONPDGQGRVYIINTASVAAFEGOVGAAYSASKGIVGMLPI 181
DB 118 TGAFLVLAWSKMTQK-----YGRIVTASVAGVGPNNMAVYASGALITALET 170
QY 182 IARDLAPIGIRVMTIAPGLF-----GTPPLTSLPEKVSNFLASOVPPSR 225
DB 171 AALDLAPYIRNANALSPGIMGEMERQVVELQAKVGSQYSTDKVVAAQMGISVPR-R 229
QY 226 RUGDPAEVAHLVQAI--ENPFLNGEVRIRLDG 255
DB 230 RYGDINEIPGVAFLLGDDSSPMTGVNPIAG 261

RESULT 22
US-09-802-853-6
Sequence 6, Application US/09802853
Patent No. US20010034049A1
GENERAL INFORMATION:
APPLICANT: SUGIYAMA, MASAKAZU
APPLICANT: TONOUCHI, NAORO
APPLICANT: SUZUKI, SHUNICHI
APPLICANT: YOKOZUKI, KENZO
TITLE OF INVENTION: XYLIOTOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THERE
FILE REFERENCE: 0010-1024-0
CURRENT APPLICATION NUMBER: US/09/802,853
CURRENT FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 09/363,189
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: JP10-216047
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 262
TYPE: PRT

ORGANISM: Gluconobacter oxydans
US-09-802-853-6

Query Match 22.5%; Score 293.5; DB 10; Length 262;
Best Local Similarity 31.6%; Pred. No. 8,9e-19;
Matches 86; Conservative 42; Mismatches 109; Indels 35; Gaps 7;

QY 6 RSVGLVAVITGASGLGATAEPLVAGASAVLLDPNNG---GEAOKLNNCVFAP 62
DB 3 KRFNGKCVLTGAGNIGLALPLAEGRALALDDNRLKAEKSVKREVEARSY 62
QY 63 ADVTSEKDVCTALALAKGKTGRVDVAVNCAGIAVASTYMLKKGQTHLEDFORVLDVNL 122
DB 63 CDVTSEAVITGVSVVRDFGKIDFLFNNGAYQGA----FAVQDYPSPDFAFRLITNV 117
QY 123 MGFNVIRLVAGEM-GONEPDQGGQGRVITNTASVAPEGOVGOAAYASAKGIVGMLP 181
DB 118 TGAHVLEKAVSRQITON-----YGRVNTASMAVYKQPPNMAAGAKGAILALTEF 170
QY 182 IARDLAPIGIRVMTIAPGLF-----GPELTLSPKVSNFLASQVFPFS 225
DB 171 AALDLAPYRIRVNAISPGYMGPGPMERQVELAKVGSQYFSTDPKYVAQOMIGSVPM-R 229
QY 226 RLGDPAEYAHLYQ--ENPELNGEVIKLDG 255
DB 230 RYGDINELPGVAVFLADDSSEMTGVNLPJAG 261

RESULT 23

US-09-815-242-10126

Sequence 10126, Application US/09815242

Patent No. US2002061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-07-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: fastseq for Windows version 4.0

SEQ ID NO 10126

LENGTH: 244

TYPE: PRT

ORGANISM: Escherichia coli

US-09-815-242-10126

Query Match 22.4%; Score 291.5; DB 10; Length 244;
Best Local Similarity 30.0%; Pred. No. 1.2e-18;
Matches 76; Conservative 50; Mismatches 112; Indels 15; Gaps 4;

QY 9 KGLVAVITGASGLGATAEPLVAGASAVLLDPNNGEAGAKKLGNNCVFAPADVTSE 68

DB 4 EGRKIALVTGASRGIGRAIETLARGAKVIGTATSENGAQALSDYLGANGKMLNVTDP 63
QY 69 KVOGTALALAKKFGGVNDVAVNCAGIAVASTYMLKKGQTHLEDFORVLDVNL 128
DB 64 ASIESVLEKIRAEFGVVDILVNNAGITRDNLMRKD-----EEMNDIIEITNLSSVRL 117
QY 129 IRLVAGEMQNEPDQGGQGRVITNTASVAPEGOVGOAAYASAKGIVGMLPPIARDAP 188
DB 118 SKAVMAAMKK-----RHGRITITGSVYGVGNGQANVAAKAGLIGFSKSLAREVAS 171
QY 189 IGRVMTIAPGLFPELTLSPKVSNFLASQVFPFSRLGDPAEYAHLYQ--ATLENFL 246
DB 172 RGTIVVAVAPGLETDMTRALSDDQRAIGLAVP-AGRUGAQETANNVAFILASDEAAYI 230
QY 247 NGEVIRLDGAIRM 259
DB 231 TGETLHVNGMYM 243

RESULT 24

US-09-978-295A-468

Sequence 468, Application US/09978295A

Patent No. US2002015606A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Fliviaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerlitsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kijavyn, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William J.

TITLE OF INVENTION: Acids and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2630PIC11

CURRENT APPLICATION NUMBER: US/09/978,295A

CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/077450

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077641

PRIOR FILING DATE: 1998-03-11

Page 12

PRIOR FILING DATE: 1998-04-21	PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22	PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22	PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22	PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22	PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23	PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27	PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28	PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083570
PRIOR FILING DATE: 1998-04-30	PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30	PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-06	PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06	PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06	PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084643
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PRIOR FILING DATE: 1998-05-15	PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15	PRIOR APPLICATION NUMBER: 60/085573
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Thu Jun 26 06:55:06 2003

us-09-931-186-23.rapb

Page 13

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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      22.3%; Score 290.5; DB 9; Length 270;
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Matches 85; Conservative 43; Mismatches 114; Indels 21; Gaps 8;

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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Shetman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James.
; APPLICANT: Paoli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
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; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC27
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Page 14

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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 22.3%; Score 290.5; DB 9; Length 270;
Best Local Similarity 32.3%; Pred. No. 1.7e-18;
Matches 85; Conservative 43; Mismatches 114; Indels 21; Gaps 8;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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SUMMARIES

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ALIGNMENTS

RESULT 1

US-08-815-225-2

; Sequence 2, Application US/08815225
; Patent No. 6268479

; GENERAL INFORMATION:

; APPLICANT: Stern, David M.

; APPLICANT: Yan, Shi Du

; TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE

; TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING

; TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: U.S.A.

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/815,225

; FILING DATE: 12-MAR-1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 0575/55209

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 278-0400

; TELEFAX: (212) 391-0525

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 261 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-815-225-2

Query Match 99.6%; Score 1299; DB 4; Length 261;

Best Local Similarity 99.6%; Pred. No. 1,1e-135;

Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MAAACRSYKGLVAVITGGASGLGATAEKLVGOGASAVLLDLPNSGGEQAQKLGNNCF 60
DB 1 MAAACRSYKGLVAVITGGASGLGATAEKLVGOGASAVLLDLPNSGGEQAQKLGNNCF 60
QY 61 APADVSEKDVQOTALAKGKFGKRDVAVNCGIAVASKTYNLKKGQTHLEDFQRYLDV 120
DB 61 APADVSEKDVQOTALAKGKFGKRDVAVNCGIAVASKTYNLKKGQTHLEDFQRYLDV 120
QY 121 NLMGTFNVIRLVAGEMGNEDPDGGQGVYIINTASVAAREGQVGAAYASASGKGIYGMTL 180
DB 121 NLMGTFNVIRLVAGEMGNEDPDGGQGVYIINTASVAAREGQVGAAYASASGKGIYGMTL 180
QY 181 PIARDLAPIGIRMTIAPGLFTPLTSLPEKVSNTLASOVFPSPRLGDPAEYAHLYQAI 240
DB 181 PIARDLAPIGIRMTIAPGLFTPLTSLPEKVSNTLASOVFPSPRLGDPAEYAHLYQAI 240
QY 241 IENPFLNGEYIRLDGAIRMOP 261
DB 241 IENPFLNGEYIRLDGAIRMOP 261
```

RESULT 2

```
US-08-815-225-3
; Sequence 3, Application US/08815225
; Patent No. 6268479
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE
; TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING
; TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,225
; FILING DATE: 12-MAR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/55209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-815-225-3
```

Query Match 99.6%; Score 1299; DB 4; Length 261;

Best Local Similarity 99.6%; Pred. No. 1,1e-135;

Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MAAACRSYKGLVAVITGGASGLGATAEKLVGOGASAVLLDLPNSGGEQAQKLGNNCF 60
DB 1 MAAACRSYKGLVAVITGGASGLGATAEKLVGOGASAVLLDLPNSGGEQAQKLGNNCF 60
QY 61 APADVSEKDVQOTALAKGKFGKRDVAVNCGIAVASKTYNLKKGQTHLEDFQRYLDV 120
DB 61 APADVSEKDVQOTALAKGKFGKRDVAVNCGIAVASKTYNLKKGQTHLEDFQRYLDV 120
QY 121 NLMGTFNVIRLVAGEMGNEDPDGGQGVYIINTASVAAREGQVGAAYASASGKGIYGMTL 180
DB 121 NLMGTFNVIRLVAGEMGNEDPDGGQGVYIINTASVAAREGQVGAAYASASGKGIYGMTL 180
QY 181 PIARDLAPIGIRMTIAPGLFTPLTSLPEKVSNTLASOVFPSPRLGDPAEYAHLYQAI 240
DB 181 PIARDLAPIGIRMTIAPGLFTPLTSLPEKVSNTLASOVFPSPRLGDPAEYAHLYQAI 240
QY 241 IENPFLNGEYIRLDGAIRMOP 261
DB 241 IENPFLNGEYIRLDGAIRMOP 261
```

```
RESULT 3
US-09-347-878-50
; Sequence 50, Application US/09347878C
; Patent No. 6376210
; GENERAL INFORMATION:
; APPLICANT: Yuan, Chong
```

;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
;; FILE REFERENCE: 25885-1651
;; CURRENT APPLICATION NUMBER: US/09/347,878C
;; CURRENT FILING DATE: 1999-07-06
;; NUMBER OF SEQ ID NOS: 75
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 50
;; LENGTH: 261
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-347-878-50

Query Match 99.6%; Score 1299; DB 4; Length 261;
Best Local Similarity 99.6%; Pred. No. 1.1e-135;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAACRSVKGLVAVITGGASGLGATAERLVGGASAVLLDLPNSGGEAOKKLGNNCYF 60
DB 1 MAACRSVKGLVAVITGGASGLGATAERLVGGASAVLLDLPNSGGEAOKKLGNNCYF 60
QY 61 APADVTSEKDVOTATLAKGKGRVDVAVNCAGIAVASKTYNLKGGOTHTLEDFOFVLDY 120
DB 61 APADVTSEKDVOTATLAKGKGRVDVAVNCAGIAVASKTYNLKGGOTHTLEDFOFVLDY 120
QY 121 NLKGFENVIRLVAGEMQNEPDGQGGQGVIIINTASVAAFEQVGOAAYASASKGIVGM 180
DB 121 NLKGFENVIRLVAGEMQNEPDGQGGQGVIIINTASVAAFEQVGOAAYASASKGIVGM 180
QY 181 PIADLAPIGIRVMTIAPGLFGLTSLPEKVSNFLASQVPPSRIGDPAEYAHLYQAI 240
DB 181 PIADLAPIGIRVMTIAPGLFGLTSLPEKVSNFLASQVPPSRIGDPAEYAHLYQAI 240
QY 241 IENPLNGEVIIRLDGAIRMQP 261
DB 241 IENPLNGEVIIRLDGAIRMQP 261

RESULT 4
US-08-980-832-41
;; Sequence 41, Application US/08980832B
;; Patent No. 6291204
;; GENERAL INFORMATION:
;; APPLICANT: Pasamontes, Luis
;; TITLE OF INVENTION: Improved Fermentative Carotenoid Production
;; FILE REFERENCE: Improved Fermentative Carotenoid
;; CURRENT APPLICATION NUMBER: US/08/980,832B
;; CURRENT FILING DATE: 1997-12-01
;; NUMBER OF SEQ ID NOS: 66
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 41
;; LENGTH: 388
;; TYPE: PRT
;; ORGANISM: Flavobacterium sp. R1534
US-08-980-832-41

Query Match 51.2%; Score 667.5; DB 4; Length 388;
Best Local Similarity 55.5%; Pred. No. 1.7e-65;
Matches 141; Conservative 35; Mismatches 69; Indels 9; Gaps 3;
QY 8 VKGLVAVITGGASGLGATAERLVGGASAVLLDLPNSGGEAOKKLGNNCYFAPADYTS 67
DB 143 IEGRVFVTVGAASARMLAOGAKVYLADL-----AEPKDAPEGAVHAACDYTD 196
QY 68 EKDVOTATLAKGKGRVDVAVNCAGIAVASKTYNLKGGOTHTLEDFOFVLDYNLKGFENV 127
DB 197 ATAACTATATLADRGRDGLVNCAGIAPALERM--LGDDGPHGJDSFAVATINLIGSFN 254
QY 128 VIRLVAGEMQNEPDGQGGQGVIIINTASVAAFEQVGOAAYASASKGIVGMITPIARDLA 187
DB 255 MARLAFAAMARNEPVR-GERGVIVNTASIAQDDQIGOVAVAAASAGVAGKTLPMAROLA 313
QY 188 PIGIRVMTIAPGLFGLTSLPEKVSNFLASQVPPSRIGDPAEYAHLYQAI IENPLN 247

DB 314 RHGIRVMTIAPGLFGLTSLPEKVSNFLASQVPPSRIGDPAEYAHLYQAI IENPLN 247
QY 248 GEVIRLDGAIRMQP 261
DB 374 GEVIRLDGAIRMQP 387

RESULT 5
US-09-239-052-2
;; Sequence 2, Application US/09239052
;; Patent No. 6346395
;; GENERAL INFORMATION:
;; APPLICANT: Holmes, David J.
;; APPLICANT: Zhong, Yixi
;; APPLICANT: Dedouck, Christine
;; APPLICANT: Jaworski, Deborah D.
;; APPLICANT: Wang, Min
;; APPLICANT: Warren, Richard L.
;; APPLICANT: Kosmatka, Anna L.
;; APPLICANT: McDevitt, Damien
;; APPLICANT: Ingraham, Karen A.
;; APPLICANT: Chalke, Allison F.
;; APPLICANT: So, Chi Young
;; APPLICANT: Wallis, Nicola G.
;; APPLICANT: Pearson, Stewart C.
;; TITLE OF INVENTION: FastSeq for Windows Version 3.0
;; FILE REFERENCE: GM10191
;; CURRENT APPLICATION NUMBER: US/09/239,052
;; CURRENT FILING DATE: 1999-01-27
;; NUMBER OF SEQ ID NOS: 2
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 2
;; LENGTH: 243
;; TYPE: PRT
;; ORGANISM: Streptococcus pneumoniae
US-09-239-052-2

Query Match 25.3%; Score 329.5; DB 4; Length 243;
Best Local Similarity 35.1%; Pred. No. 2.2e-28;
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;
QY 15 ITGASGLGATAERLVGGASAVLLDLPNSGGE-----AOKKLGNNCYFAPADYTS 68
DB 10 ITSSSGSIGLAIHAKRAQAGANTVL-----NSRGATSELLAEPSNTGIVYVTSQDVSD 65
QY 69 KDVOATLALAKGKGRVDVAVNCAGIAVASKTYNLKGGOTHTLEDFOFVLDYNLKGFENV 128
DB 66 ADAKRMIDQAIABELGSDVLYNNAGI--TODTLMKLM---TEADPEKYLKYNLGAQAFNM 119
QY 129 IRLVAGEMQNEPDGQGGQGVIIINTASVAAFEQVGOAAYASASKGIVGMTPPIARDLAP 188
DB 120 TQSVL-----KPMKARBEAIIIMSSVVGKMGNTQANTASKACLIFFTSVAREVAS 173
QY 189 IGRVMTIAPGLFGLTSLPEKVSNFLASQVPPSRIGDPAEYAHLYQAI IENPLN 248
DB 174 RNRVNVNTAGMESDMTALISDKIKETALQAPM-KERGOAQVADVLDVFLAQQGVYING 232
QY 249 EVIRLDGAIRMQP 259
DB 233 QVIAIDGGLSM 243

RESULT 6
US-08-815-225-4
;; Sequence 4, Application US/08815225
;; Patent No. 6268479
;; GENERAL INFORMATION:
;; APPLICANT: Stern, David M.
;; APPLICANT: Yan, Shi Du
;; TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE
;; TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING
;; TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS

```

NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,225
FILING DATE: 12-MAR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/55209
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-815-225-4

Query Match      23.2%; Score 302; DB 4; Length 255;
Best Local Similarity 33.6%; Pred. No. 2,7e-25;
Matches 85; Conservative 47; Mismatches 101; Indels 20; Gaps 8;

QY 8 VKGLVAVITGSGAGSLGATAEARLYVGCGASAVLLDPRNSGGEAQAARKGNVCVAPADYTS 67
DB 4 LSGRTVITGSGARLGAEARQAVAGARVYLDVDEBGAATREAGDARQOHDVYTI 63
QY 68 EKDQOTALALAKGFGFGRVDVAVNCAGIYASVSKTYNKKQTHLEDFORYLDVNLGTFN 127
DB 64 EEDQGVYAVAREBFGSVVDGLVNNAGISTGMFL-----ETESVERERKVVLDNLGVFI 117
QY 128 VIRIYAGEMQNEPDGQGVITINTASVAAFEGQVQAAVSASKSGIVGMLPIARDLA 187
DB 118 GMKTVIPAM---KDAAG--GSTVNISSAAGLMGLALTSSGASKMGVRLSKLAAYELG 171
QY 188 PIGIRVMTIAPGLFGTPLL--TSLPERVSNFLASQVFPFSLG--DPAEYAHLYOALIE-- 242
DB 172 TDRIRVNSVHGMQMTYTMATETGIRGEGNV--PNTFM--GRVGNPEIAGVAYKLLSDT 228
QY 243 NPLFNGEYIRLDG 255
DB 229 SSYVTGAEALVDG 241

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RESULT 7
US-08-440-856A-4
Sequence 4, Application US/08440856A
Patent No. 5750873
GENERAL INFORMATION:
APPLICANT: DELAPORTA, STEPHEN L.
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVE. N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA

```

```

ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,856A
FILING DATE: 15-MAY-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 05463-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1517
TELEFAX: (202) 887-0763
TELEX: 706141
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-440-856A-4

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Query Match      22.9%; Score 298.5; DB 1; Length 333;
Best Local Similarity 32.5%; Pred. No. 9,9e-25;
Matches 92; Conservative 46; Mismatches 106; Indels 39; Gaps 5;

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QY 6 RSVKGLVAVITGSGAGSLGATAEARLYVGCGASAVLLDPRNSGGEAQAARKGNVCVAPADY 65
DB 50 KRLGKGVAVITGSGAGSLGATAEARLYVGCGASAVLLDPRNSGGEAQAARKGNVCVAPADY 109
QY 66 TEKEDOTALALAKGFGFGRVDVAVNCAGIYASVSKTYNKKQTHLEDFORYLDVNLGTFN 125
DB 110 SYBEDERAVERAAYRAGYLDVLCNNAGV--LGRQTRAKSILSFAGEFDRVLRVNALGA 168
QY 126 FNVIRIYAGEMQNEPDGQGVITINTASVAAFEGQVQAAVSASKSGIVGMLPIARD 185
DB 169 ALGMRHAALAKTOR-----RAGSITSVASVAGVIGLGPATYTSKHAIVGLTKNACE 222
QY 186 LAPIGIRVMTIAPGLFGTPLL-----TSLP-----EKVS 214
DB 223 LGHGIRVNCISPFVATPMLLNAMKQGDASTADADADIDLDIAYPSDQEVEMEEVY 282
QY 215 NPLASQVFPFSLGDPAEYAHLYOALIEPFLNGEYIRLDGAI 257
DB 283 RGLATLKGATLRPRDIAB--AALFLASDDSRYSIGNLVVDGCV 324

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```

RESULT 8
US-09-134-001C-4512
Sequence 4512, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4512
LENGTH: 263
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4512

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Page 5

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US-08-793-035-9
Query Match      22.6%  Score 295;  DB 3;  Length 315;
Best Local Similarity 30.5%;  Fred. No. 2,2e-24;
Matches 80;  Conservative 44;  Mismatches 116;  Indels 22;  Gaps 6

QY      4  ACRSVKGLAVVITGASGLGLATERLVGGQASAVLLDLPNSGGEA-----QAKLGNNC 58
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      66  AWPKEVSPVVVITGASRGIGRAIALST-GRKGCELVNVYARSAAKEEVSQKLEAAGQA 124

QY      59  VAPADYTEKRVQFALALAKGRGRDVANVNCGLIVASKTINLAKGQTHLLEDPQRL 118
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      125  ITFGGVSEAEVVEEMMTALIDAGMTIDVYVNNNGITRDLLIRMKSC-----WDEVI 178

QY      119  DVNLMTGFENVIRLVAGEKQNEPDQGGQVYIINTASVAAFEQGVQAAYSASKGIVGM 178
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      179  DNLITGVEFCTQAAATKIMRK-----RKGRIIIASVYVLLINIQAAVAAKAGVIGF 232

QY      179  TLTPIDLAPIGIRMTIAPGLFEGPLITSPEKVSFNLASQVPPSRGDPAEVAHLYQ 238
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      233  SKIAAREGASRNINNVYCPGFIASDMTAKIGEMERKILITLPL-GRYGQPDVAQVIE 291

QY      239  ALEND---FLNGEVIRLDGAI 257

```

RESULT 10
US-08-793-035-10
Sequence 10, Application US/08793035
Patent No. 6011201
GENERAL INFORMATION:
APPLICANT: Slabas, Antoni R.
APPLICANT: White, Andrew
APPLICANT: Chase, Dianne
APPLICANT: Elborough, Keiran
APPLICANT: Fentem, Phillip A.
TITLE OF INVENTION: B-ketacyl ACP Reductase Genes From
TITLE OF INVENTION: Brassica Napus
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentia Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,035
FILING DATE: 28-JUL-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9414622.2
FILING DATE: 20-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB95/01678
FILING DATE: 17-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kammerer, Patricia A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: M08T.132
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713.787.1400
TELEFAX: 713.787.1440
INFORMATION FOR SEQ. ID NO.: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
TYPE: amino acid

Thu Jun 26 06:55:05 2003

us-09-931-186-23.ral

Page 6

STRANDEDNESS: single
TOPOLOGY: linear
US-08-793-035-10

Query Match 22.6%; Score 295; DB 3; Length 315;
Best Local Similarity 30.5%; Pred. No. 2.2e-24;
Matches 80; Conservative 44; Mismatches 115; Indels 22; Gaps 6;

QY 4 ACSVAGIVAVITGASGLGATAEERLVGOGASAVLLDLPNSGGEA-----GAKKIGNNC 58
DB 66 AVKRESPVAVVVGASGIGKATATSL-GRAGCKVAVNARSKEAEVSKOLEAVGGA 124
QY 59 VFAPADYSEKDYOTALALAKGFGVDVAVNCAGIYASAKTYNKKQTHLEDFORVL 118
DB 125 ITFGDYSKADYEAAMKKTADAMGFTIDVYVNNAGITRDTLIRMKKSQ-----WDEVY 178
QY 119 DVNLMGFNIRLVAGMGNEPDGOGRCVITNTASVAFEGVGOAAYASAKGIVGM 178
DB 179 DLNLTGVFLCTQAAATKIMRK-----RKGRITINIASVVGIGINIGQANTAAKAGVIGP 232
QY 179 TLPIARDLAPIGIRVMTIAPGLFTPLLSLPEKVENFLASQVFPFSRLGDPAEVAHLVQ 238
DB 233 SKTARAGCASRNINNVVYCPFLASDWTAKLGEDMEKILGITPL-GRYGQPDVAGVIE 291
QY 239 AITENP---FLNGEVITLDCAI 257
DB 292 FLALSPASVYITGOAFTIDGI 313

RESULT 11
US-09-363-189B-6
Sequence 6, Application US/09363189B
Patent No. 6242228
GENERAL INFORMATION:
APPLICANT: SUGIYAMA, MASAKAZU
APPLICANT: TOMODUCHI, NAOTO
APPLICANT: SUZUKI, SHUNICHI
APPLICANT: YOKOZAKI, KENZO
TITLE OF INVENTION: XYTITOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF
FILE REFERENCE: 0010-1024-0
CURRENT APPLICATION NUMBER: US/09/363, 189B
CURRENT FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: JP10-216047
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 262
TYPE: PRT
ORGANISM: Gluconobacter oxydans
US-09-363-189B-6

Query Match 22.5%; Score 293.5; DB 4; Length 262;
Best Local Similarity 31.6%; Pred. No. 2.4e-24;
Matches 86; Conservative 42; Mismatches 109; Indels 35; Gaps 7;

QY 6 RSVGGLVAVITGASGLGATAEERLVGOGASAVLLDLPNSG--GEAOKKLGNNCVFAP 62
DB 3 KKNFGKVLVAGAGNIGLATALRLAEGRITALLDMNREALEKAESVREKVEARSYV 62
QY 63 ADVYSEKDYOTALALAKGFGVDVAVNCAGIYASAKTYNKKQTHLEDFORVLVNL 122
DB 63 CDVYSEAVVITGVSVDVDFGKIDFLFNAGYGA-----FAPVDYPSDFAVVLTINV 117
QY 123 MGFENVIRLVAGEM-GONEPDGOGRCVITNTASVAFEGVGOAAYASAKGIVGTLPL 181
DB 118 TGAHFVLAASVRKMTGN-----YGRVITVASMAGVKGPPNMAAAGASGAILALLET 170
QY 182 IARDLAPIGIRVMTIAPGLF-----GIPPLTSLPEKVSNFLASQVFPFS 225
DB 171 AALDLAPYINIRVNAISPGYMGPGEMERQVELQAKVQSQYFSTDPKVVAAQMGISVPM-R 229
QY 226 RLGDPAEVAHLVQAIT--ENPFLNGEVITRLDG 255

DB 230 RYGDINELRPGVAVFLLGDSSFFMTGVNLPING 261

RESULT 12
US-08-375-962B-13
Sequence 13, Application US/08375962B
Patent No. 5731195

GENERAL INFORMATION:
APPLICANT: STIMON, ANDRAS; HELLMAN, ULF; WERNSTEDT,
APPLICANT: CRISTER, ERIKSSON, ULF.
TITLE OF INVENTION: Isolated Nucleic Acid Molecule
TITLE OF INVENTION: Which Codes for A 32 kDa Protein Having 11-CIS Retinol
TITLE OF INVENTION: Dehydrogenase Activity, and Which Associates With P63,
TITLE OF INVENTION: a Portion of a Retinol Binding Protein Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect (ASCII standard)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375, 962B
FILING DATE: 20-January-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/258, 418
FILING DATE: 6-October-1994
ATTORNEY/AGENT INFORMATION:
NAME: Pasquallini, Patricia A.
REGISTRATION NUMBER: 34, 894
REFERENCE/DOCKET NUMBER: LUD 5372.1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]
NAME/KEY: reductase (FABG)
US-08-375-962B-13

Query Match 22.0%; Score 287.5; DB 1; Length 244;
Best Local Similarity 29.6%; Pred. No. 1e-23;
Matches 75; Conservative 50; Mismatches 113; Indels 15; Gaps 4;

QY 9 KGLVAVITGASGLGATAEERLVGOGASAVLLDLPNSGGEAOKKIGNNCVAPADYSE 68
DB 4 EGRALVVGASRGIGRAIETLAAAGKYGITATSNGQAISDYLGANGKGMUNVDIP 63
QY 69 KDQVOTALALAKGFGVDVAVNCAGIYASAKTYNKKQTHLEDFORVLVNLNGTFNV 128
DB 64 ASIESVLEKTRAEFGVVDILVNNAGITRDNLMRKMD-----EEMNDIETNLSVFR 117
QY 129 IRLVAGMGNEPDGOGRCVITNTASVAFEGVGOAAYASAKGIVGTLPLIARDLAP 188
DB 118 SKAVNRAAMKK-----RHGRITITSSVYGTMGNGQAVYAAKAGLILFSSKLAEVAS 171
QY 189 IGIRVMTIAPGLFTPLLSLPEKVSNFLASQVFPFSRLGDDPAEVAHLVQ--AITENP 246
DB 172 RGTIVVAVPFGLETMTALSDDPDAGITAOVP-AGRLGAQDETANAVATLASDEAAVI 230

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QY 189 IGRVMTIAPGLFETPLTSLPEKVSNTLASOVPPPSRLGDPAEYAHLYO--AIENPFL 246
Db 172 RGLIVNVVAVGFIETDTRALSDQDAGILAOVP--AGRLGAGQEIANNVAFSLASDEAYI 230
QY 247 NGEVIRLDGAIRM 259
Db 231 TGETLHVNGMGM 243

RESULT 15
US-08-937-993-13
Sequence 13, Application US/08937993
Patent No. 6399344
GENERAL INFORMATION:
APPLICANT: ERIKSSON, ULF; SIMON, ANDRAS; ROMERT, ANNA
TITLE OF INVENTION: ISOLATED PROTEINS HAVING CIS-R
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,993
FILING DATE: September 26, 1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/729,594
FILING DATE: 11-October-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/562,114
FILING DATE: 22-NO. 6399344member-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/375,962
FILING DATE: 20-January-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/258,418
FILING DATE: 10-June-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6399344man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: IUD 5517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 858-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]reductase
US-08-937-993-13

Query Match 22.0%; Score 287.5; DB 4; Length 244;
Best Local Similarity 29.6%; Pred. No. 1e-23;
Matches 75; Conservative 50; Mismatches 113; Indels 15; Gaps 4;
QY 9 KGLVAVITGASGIGLATAEERLVGOGASAVLLDPPNSGGEGAAKIGNNCVFAPADYTS 68
Db 4 EGKIALVTGASRGIRALTAETLARGKVGISTATSENGAQAISDYLGANGGLMLNTDP 63
QY 69 KDVGCTALALAKGKGRVDVAVNCAGINASTYLNLRKGGTHTLDDFORVLDVNLMGTFNV 128

Db 64 ASIESVLEKIRAEFGEVDILVNNAGITDNLIMRKD-----EEMNDIETNLSVFR 117
QY 129 IRLVAGMGONPPDGGGQGVIIINTASVAEEGQVGAASKAGIYGMTLPFIARDIAP 188
Db 118 SKAVYRAMMK-----RGRITIGSVYGTNGNGGQANVAAKAGLIGFSKSLAREVAS 171
QY 189 IGRVMTIAPGLFETPLTSLPEKVSNTLASOVPPPSRLGDPAEYAHLYO--AIENPFL 246
Db 172 RGLIVNVVAVGFIETDTRALSDQDAGILAOVP--AGRLGAGQEIANNVAFSLASDEAYI 230
QY 247 NGEVIRLDGAIRM 259
Db 231 TGETLHVNGMGM 243

RESULT 16
5229279-7
Patent No. 5229279
APPLICANT: PEOPLES, OLIVER P.; SINSKEY, ANTHONY J.
TITLE OF INVENTION: METHOD FOR PRODUCING NOVEL POLYESTER
BIOPOLYMERS
NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/556,535
FILING DATE: 13-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 67,695
FILING DATE: 29-AUG-1987
SEQ ID NO: 7
LENGTH: 246

Query Match 22.0%; Score 286.5; DB 6; Length 246;
Best Local Similarity 31.9%; Pred. No. 1.3e-23;
Matches 81; Conservative 45; Mismatches 109; Indels 19; Gaps 7;

QY 12 VAVITGASGIGLATAEERLVGOGASAVLLDPPNSGGE-----AQAKIGNNCVFAPADYTS 67
Db 5 IAYVTGGMGIGTALCOBLAKDGFYVAGCGNSPRREKWLQOKALFEDFASGYNAD 64
QY 68 EKDVOCTALALAKGKGRVDVAVNCAGIYASTYLNLRKGGTHTLDDFORVLDVNLMGTFN 127
Db 65 WDSTKAPFKVSEVGEVDVLLNNGI---TDDYFRR---WTRADMVAVIDNTLSFN 118
QY 128 VIRLVAGMGONPPDGGGQGVIIINTASVAEEGQVGAASKAGIYGMTLPFIARDIAP 187
Db 119 VTKQVIDGMA---DRGM--GRIVNISVNGKQGFQGTNTSTARAAGJHGFMLAOCYVA 172
QY 188 PIGIRVMTIAPGLFETPLTSLPEKVSNTLASOVPPPSRLGDPAEYAHLYOAI--ENPF 245
Db 173 TKGVIYNTVSPGIATDMKAIRODYLDIVATFY--KRLSPQIATSCMLWSSEBSGF 231
QY 246 NGEVIRLDGAIRM 259
Db 232 STGADFSLNGGLHM 245

RESULT 17
5512669-4
Patent No. 5512669
APPLICANT: PEOPLES, OLIVER P.; SINSKEY, ANTHONY J.
TITLE OF INVENTION: GENE ENCODING BACTERIAL ACETOACETYL-COA
REDUCTASE
NUMBER OF SEQUENCES: 7
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,667
FILING DATE: 29-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 124,570
FILING DATE: 20-SEP-1993
APPLICATION NUMBER: 944,488
FILING DATE: 03-NOV-1992
APPLICATION NUMBER: 566,535

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FILING DATE: 13-AUG-1990
APPLICATION NUMBER: 67,695
FILING DATE: 29-JUN-1987
SEQ ID NO: 4
LENGTH: 273
5512669-4

Query Match 21.6%; Score 281.5; DB 6; Length 273;
Best Local Similarity 31.5%; Pred. No. 5.5e-23;
Matches 90; Conservative 42; Mismatches 91; Indels 63; Gaps 11;

12 VAVITGASGLGATATATRLVGGASAVLLDLPNSGGEAOKKLGNNCFAPA-----63
4 VAVITGASGLGATATATRLVGGASAVLLDLPNSGGEAOKKLGNNCFAPA-----63
64 ---DVTSEKDVQATLALAKGKFGVDVAVNCAGIAVASKTYNKKGQTH--TLEDQORVL 118
52 YKMDVSSYEACVEBIAKVEADLGPIDVLVNNAGIT-----KDMFHKMTEDQNNAVI 103
119 DVNLMTGFNVT-----RLV-----AGEMGO-NEPDGGGR---GVIIIN 152
104 NTNLTLGLFNMTHPVWSGMRDRSFGRIYINISSINGOKGOMQANYSVWSGMRDRSFGRIYIN 163
153 TASVAPEGGVGOAAYASAGSGIYGMPLTARDIAPIGIRVMTIAPGLTGTPLTSLPER 212
164 ISSINGOKGOMQANYSAGSGIYGMPLTARDIAPIGIRVMTIAPGLTGTPLTSLPER 223
213 VSN-FLASQVFPSPRLGDPATAYAHV--QALIEPNPLNGEVIRLDG 255
224 VLNERIIPQIV-GRGEPDEIARIYVFLASDEAGFITGTSISANG 268

RESULT 18
US-09-134-001C-4431
Sequence 4431, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4431
LENGTH: 274
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4431

Query Match 21.6%; Score 281.5; DB 4; Length 274;
Best Local Similarity 31.7%; Pred. No. 5.6e-23;
Matches 85; Conservative 45; Mismatches 93; Indels 45; Gaps 8;

12 VAVITGASGLGATATATRLVGGASAVLLDLPNSGGEAOKKLGNNCF 60
10 IAVITGASTGICQASAVLALAEAVLALDISDLEETVQSIINDGKATAYRV-----63
61 APADVTSEKDVQATLALAKGKFGVDVAVNCAGIAVASKTYNKKGQTH--TLEDQORVL 118
64 ---DISDKOVYKOFSEKIAOEFGRVAVIFNNAGVNGA-----GRITHEPVEVEFKIM 113
119 DVNLMTGFNVTIRLVGEMGONPDGGGRIYINIASVAPEGGVGOAAYASAGSGIYGM 178
114 AVDMKGTPLVTKFLL-----PLMKKGGSITINASTSGGAADLYRSGIYNAKGVIN 166
179 TLPIARDIAPIGIRVMTIAPGLTGTPLTSLPERVSNFLASQ--VFPSPRLGDP 231
167 TSIAIEYGRNIRANALAPGTIEPLVDNLGAGTDEDEAGOTFRNOKWVTPIGRLGTPD 226

232 EXAHLV--ATLENPELNGEVIRLDGAI 257
227 EVGKLVAFLASDSSFTIGETIRIDGV 254

RESULT 19
US-09-134-001C-4825
Sequence 4825, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4825
LENGTH: 249
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4825

Query Match 21.2%; Score 276.5; DB 4; Length 249;
Best Local Similarity 29.1%; Pred. No. 1.7e-22;
Matches 74; Conservative 54; Mismatches 105; Indels 21; Gaps 6;

13 VAVITGASGLGATATATRLVGGASAVLLDLPNSGGEAOKKLGNNCFAPADYTS 67
10 ALVTGASRSGIGRISALQLAEEGVN-VAVNAGSKDAEAVBEIRAKGESFAIOANAK 68
68 EKDVQATLALAKGKFGVDVAVNCAGIAVASKTYNKKGQTHLEDQORVLDVNLMTGFN 127
69 GDEVKEMIKRVQFSVVDVAVNAGITRDNLMRKE-----QEMDVVIDTNKGVFN 122
128 VITLVAGEMQNPDPDGGGRIYINIASVAPEGGVGOAAYASAGSGIYGMPLTARDIA 187
123 CICKVPPQMLRQ-----RSGATINLTSTVGAANGPNQANVATKAGVIGLTKTARELA 176
188 PIGIRVMTIAPGLTGTPLTSLPERKYSNPLASQVPPSPRLGDPATAYAHVQAIIEN--PF 245
177 SRGIYVAVAPGFIYSDMNLALSDDKDLQDLQELPL-KRGEEDTDIANVAVFLASPKARY 235
246 LNEGVIRLDGAI 259
236 ITGQTIHVNGMTM 249

RESULT 20
US-09-238-481-2
Sequence 2, Application US/09238481
Patent No. 6110704
GENERAL INFORMATION:
APPLICANT: Huang, Jiansheng
APPLICANT: McDevitt, Damien
TITLE OF INVENTION: Fabg
FILE REFERENCE: GMI0192
CURRENT APPLICATION NUMBER: US/09/238,481
CURRENT FILING DATE: 1999-01-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 246
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-238-481-2

Query Match 20.9%; Score 272.5; DB 3; Length 246;

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Best Local Similarity 28.7%; Pred. No. 4,6e-22;
Matches 73; Conservative 57; Mismatches 103; Indels 21; Gaps 6;

QY 13 AVTGGASGIGLTAERLVGQASAVLLDLPNSGGEAQA-----KTLGNNCFAPADYTS 67
Db 7 ALVTGASRGIGRISALQLAEGYN-VAVNAGSKERAEAVEEIKAKGVDSFAIQANVAD 65
QY 68 EKDVOTATLALAKGFRGVAVNCAAGIAVASKTYNLKGGQTHLEDFORVLDVNLMTFN 127
Db 66 ADEKAMIKREYVSQFGLDVLVNNAGITRDNLMRKKE-----QEMDVIDTNLKGVTN 119
QY 128 VIRLVAGMGQNEPDGQGVYIINTASVAEFGVQGAASAKGIGVMTLPIDRLA 187
Db 120 CIQKATPQMLRQ-----RSGAIIINLSVVGAVGNPQANVATKAGVIGLTKSAARELA 173
QY 188 PIGIRVMTIAPGLFETPLTSLPEKVSNFLASQVPEPSRLGDPAEYAHLYQATITEN--PF 245
Db 174 SRGIVTAVNAPGFIVSMTALSDLEKQMLTQIPL-ARQGQDTDIANTYAFASDKAKY 232
QY 246 LNSEVIRLDGAIRM 259
Db 233 ITGQTIHVNGGMYM 246

RESULT 21
US-09-572-810A-2
Sequence 2, Application US/09572810A
Patent No. 6365387
GENERAL INFORMATION:
APPLICANT: Huang, Jianzhong
APPLICANT: McDevitt, Damien
TITLE OF INVENTION: Padg
FILE REFERENCE: GMI0192
CURRENT APPLICATION NUMBER: US/09/572,810A
CURRENT FILING DATE: 2000-05-17
PRIOR APPLICATION NUMBER: 09/238,481
PRIOR FILING DATE: 1999-01-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 246
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-572-810A-2

Query Match 20.9%; Score 272.5; DB 4; Length 246;
Best Local Similarity 28.7%; Pred. No. 4,6e-22;
Matches 73; Conservative 57; Mismatches 103; Indels 21; Gaps 6;

QY 13 AVTGGASGIGLTAERLVGQASAVLLDLPNSGGEAQA-----KTLGNNCFAPADYTS 67
Db 7 ALVTGASRGIGRISALQLAEGYN-VAVNAGSKERAEAVEEIKAKGVDSFAIQANVAD 65
QY 68 EKDVOTATLALAKGFRGVAVNCAAGIAVASKTYNLKGGQTHLEDFORVLDVNLMTFN 127
Db 66 ADEKAMIKREYVSQFGLDVLVNNAGITRDNLMRKKE-----QEMDVIDTNLKGVTN 119
QY 128 VIRLVAGMGQNEPDGQGVYIINTASVAEFGVQGAASAKGIGVMTLPIDRLA 187
Db 120 CIQKATPQMLRQ-----RSGAIIINLSVVGAVGNPQANVATKAGVIGLTKSAARELA 173
QY 188 PIGIRVMTIAPGLFETPLTSLPEKVSNFLASQVPEPSRLGDPAEYAHLYQATITEN--PF 245
Db 174 SRGIVTAVNAPGFIVSMTALSDLEKQMLTQIPL-ARQGQDTDIANTYAFASDKAKY 232
QY 246 LNSEVIRLDGAIRM 259
Db 233 ITGQTIHVNGGMYM 246

RESULT 22
US-09-134-001C-4397
Sequence 4397, Application US/09134001C

Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4397
LENGTH: 231
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4397

Query Match 20.6%; Score 269; DB 4; Length 231;
Best Local Similarity 33.3%; Pred. No. 1e-21;
Matches 66; Conservative 39; Mismatches 81; Indels 12; Gaps 2;

QY 8 VKGIVAVITGGASGIGLTAERLVGQASAVLLDLPNSGGEAQAARLGNNGCFAPADYTS 67
Db 5 VKEKAVAVITGGASGIGLTAERLVGQASAVLLDLPNSGGEAQAARLGNNGCFAPADYTS 64
QY 68 EKDVOTATLALAKGFRGVAVNCAAGIAVASKTYNLKGGQTHLEDFORVLDVNLMTFN 127
Db 65 KSNIDMLKRAVIDHGHGDIIVNAGSGLSKITD-----YVWQMDTMDVNTKGLH 118
QY 128 VIRLVAGMGQNEPDGQGVYIINTASVAEFGVQGAASAKGIGVMTLPIDRLA 187
Db 119 VLGATILPYLLKQ-----SSGHIINLASVSGPEPKTNAYGATATAAIIHQSLKELA 172
QY 188 PIGIRVMTIAPGLFETPL 205
Db 173 RTGVKVTISPGWVDPIM 190

RESULT 23
US-09-504-358-14
Sequence 14, Application US/09504358
Patent No. 6365376
GENERAL INFORMATION:
APPLICANT: Rouviere, Pierre E.
APPLICANT: Brostowicz, Patricia C.
TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIATE
FILE REFERENCE: BC1001 US NA
CURRENT APPLICATION NUMBER: US/09/504,358
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 60/120,702
PRIOR FILING DATE: 1999-February-19
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Microsoft Office 97
SEQ ID NO 14
LENGTH: 256
TYPE: PRT
ORGANISM: Brevibacterium sp HCU
US-09-504-358-14

Query Match 20.6%; Score 269; DB 4; Length 256;
Best Local Similarity 31.3%; Pred. No. 1.2e-21;
Matches 83; Conservative 41; Mismatches 113; Indels 28; Gaps 9;

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QY 125 TENVIRLVAGEMQNEPDGQGRGVITINTASVAAFEGOVGOAAYSASKGIYGMPLPIAR 184
DB 119 VEFMTKHCIPYEQ---AGG--GATVNFASIVGLVSOELTPYHAKAGVAVALTRODAP 172
QY 185 DLAPIGIRVMTIAPGIFGTPILTLSTL---PEKVSNF---LASQVPPPSRLGDPAEY--AH 235
DB 173 TYGPSNIRVAVNAVAPGILITPLVKELESGRDPDGLDTKLMGAHPL--GAVGTPEEVAAT 231
QY 236 LVQAIENPFLNGEVRIRLDGAIKMQ 260
DB 232 LFLASEASFITGAVLPVDGQYTRQ 256

RESULT 24
US-09-954-314-14
Sequence 14, Application US/09954314
Patent No. 6465224
GENERAL INFORMATION:
APPLICANT: Rouviere, Pierre E.
TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIATES
FILE REFERENCE: BC1001 US NA
CURRENT APPLICATION NUMBER: US/09/954,314
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/120,702
PRIOR FILING DATE: 1999-February-19
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Microsoft Office 97
SEQ ID NO 14
LENGTH: 256
TYPE: PRT
ORGANISM: Brevibacterium sp HCU
US-09-954-314-14

Query Match 20.6%; Score 269; DB 4; Length 256;
Best Local Similarity 31.3%; Pred. No. 1.2e-21;
Matches 83; Conservative 41; Mismatches 113; Indels 28; Gaps 9;

QY 10 GLVAVITGASGLATAEERLVGQASAVLLDLPNSGGEQAARKL---GNMCYFAPADVT 66
DB 6 GKVAVITGGAAGMRIGSELVYASEGAQVAVVDVNEDEGRATADAIASAGGVANYMKLDVS 65
QY 67 SEDVQFALALAKKFERVAVNAGIAVASKTYNKKQGTITLE--DEQRYLDVNMKG 124
DB 66 DESVEVELVSDIAKRGAIIVLVNMGVGTADK-----PTHEIDRIDDLVLSVDVK 118
QY 125 TENVIRLVAGEMQNEPDGQGRGVITINTASVAAFEGOVGOAAYSASKGIYGMPLPIAR 184
DB 119 VEFMTKHCIPYEQ---AGG--GATVNFASIVGLVSOELTPYHAKAGVAVALTRODAP 172
QY 185 DLAPIGIRVMTIAPGIFGTPILTLSTL---PEKVSNF---LASQVPPPSRLGDPAEY--AH 235
DB 173 TYGPSNIRVAVNAVAPGILITPLVKELESGRDPDGLDTKLMGAHPL--GAVGTPEEVAAT 231
QY 236 LVQAIENPFLNGEVRIRLDGAIKMQ 260
DB 232 LFLASEASFITGAVLPVDGQYTRQ 256

RESULT 25
US-08-858-207A-270
Sequence 270, Application US/08858207A
Patent No. 6348328
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gamm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 270:
SEQUENCE CHARACTERISTICS:
LENGTH: 186 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6348328e
US-08-858-207A-270

Query Match 20.6%; Score 268; DB 4; Length 186;
Best Local Similarity 38.7%; Pred. No. 9.4e-22;
Matches 74; Conservative 23; Mismatches 72; Indels 22; Gaps 5;

QY 15 ITGASGLATAEERLVGQASAVLLDLPNSGGE-----AQARKGNMCYFAPADVTSE 68
DB 10 ITGSSRGIGLAIYHAKFAQGANIVL-----NSRGAISEELAEFSNYGKIVPISGSDVSDF 65
QY 69 KQVQFALALAKKFERVAVNAGIAVASKTYNKKQGTITLE--DEQRYLDVNMKG 128
DB 66 ADARKMTDQAIKELSGVDVLVNNGI--TDTLMKLM---TEADFEKVLKVNLTGAENM 119
QY 129 IRLVAGEMQNEPDGQGRGVITINTASVAAFEGOVGOAAYSASKGIYGMPLPIARDLAP 188
DB 120 TQSVL-----KPMKAKARGAIIINSSVYGLMGINIGQANYASKAGLITGFKSVAREVAS 173
QY 189 IGIRVMTIAPG 199
DB 174 RIRVAVIAPG 184

Search completed: June 23, 2003, 14:35:45
Job time: 14.1667 secs

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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:19:21 ; Search time 39.6667 Seconds
(without alignments)
876.767 Million cell updates/sec

Title: US-09-931-186-23

Perfect score: 1304

Sequence: 1 MAACRSVKGAVITGAS.....ENPLNGEVRIDGAINWQ 261

Scoring table:

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Gapop 10.0 , Gapept 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

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2: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1981.DAT:*
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8: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/genesep-emb1/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/genesep-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/genesep-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1299	99.6	261	19	AAW71471
2	1146	87.9	260	20	AAV32239
3	1136	87.1	227	20	AAW67934
4	910	69.8	255	22	ABB62988
5	667.5	51.2	388	18	AAW06513
6	364.5	28.0	244	23	ABP28011
7	354	27.1	243	23	ABP27345
8	329.5	25.3	243	19	AAW80670
9	329.5	25.3	243	21	AAW15706
10	329.5	25.3	243	22	AAU37767

11	329.5	25.3	243	22	AAU37988	Streptococcus pneu
12	328.5	25.2	243	22	AAW01032	CPE 35 protein seq
13	327.5	25.1	243	22	ABW54087	Lactococcus lactis
14	321.5	24.7	245	22	AAU55328	Enterococcus faeca
15	317	24.3	257	22	AAU28344	Novel human secret
16	314	24.1	237	22	AAW50255	Human dehydrogenas
17	313.5	24.0	248	21	AAV54422	Amino acid sequenc
18	313.5	24.0	241	22	AAW63937	Purative P. abysci
19	312	23.9	237	22	AAU28156	Novel human secret
20	312	23.9	237	22	AAW19928	Human oxidoreducta
21	306.5	23.5	247	22	ABW48892	Listeria monocytog
22	303	23.2	247	21	AAV95746	Bacillus megaterium
23	300.5	23.0	288	22	AAU28296	Novel human secret
24	295	22.6	263	23	ABP39667	Staphylococcus epi
25	295	22.6	315	17	AAW89323	Rape leaf beta-ket
26	295	22.6	315	17	AAW89322	Rape seed beta-ket
27	294.5	22.6	267	22	AAW87459	Levodione reductas
28	294	22.5	262	22	AAW63032	S. epidermidis ope
29	293.5	22.5	262	22	AAW66337	G. suboxydans DSM
30	291.5	22.4	244	21	AAV54421	Amino acid sequenc
31	291.5	22.4	244	22	AAU34533	E. coli cellular p
32	290.5	22.3	270	20	AAV41761	Human PRO474 (UNO5
33	290.5	22.3	270	21	AAW44317	Human PRO474 prote
34	290.5	22.3	270	21	AAW24056	Human PRO474 prote
35	290.5	22.3	270	22	AAU28108	Novel human secret
36	290.5	22.3	279	22	AAU18296	Human endocrine po
37	290.5	22.3	303	23	ABW82624	Heridically activ
38	289.5	22.2	262	21	AAV44578	Xytilol dehydrogen
39	287.5	22.0	246	12	AAW10974	Acetocetyl CoA re
40	287.5	22.0	277	21	AAV54415	Secoisolaricresin
41	287	22.0	263	22	AAU58489	Salmonella typhi c
42	286.5	22.0	246	10	AAW94157	Acetyl-CoA reducta
43	286.5	22.0	246	10	AAW32182	Sequence encoded b
44	286.5	22.0	246	20	AAV43310	Acetocetyl-CoA re
45	286.5	22.0	246	21	AAV54423	Amino acid sequenc
46	286.5	22.0	246	21	AAW19611	Ralstonia eutropha
47	286.5	22.0	270	21	AAW42558	Human ORF5 ORF232
48	286.5	22.0	329	16	AAW1334	Acetyl-CoA-reducta
49	284.5	21.8	253	23	ABW54214	Lactococcus lactis
50	283.5	21.7	306	22	AAW81644	S. epidermidis ope
51	283	21.7	280	23	ABW82449	Heridically activ
52	281.5	21.6	273	10	AAW94155	Acetyl-CoA reducta
53	281.5	21.6	274	23	ABP39585	Staphylococcus epi
54	281	21.5	258	22	AAW32682	C glutamic prote
55	281	21.5	258	22	AAW9361	Cornebacterium gl
56	280.5	21.5	254	22	AAW49737	Protein with acety
57	278.5	21.4	241	12	AAW10679	Acetocetyl CoA re
58	277.5	21.3	242	12	AAW59280	Propionibacterium
59	277	21.2	244	22	AAW81318	Human AFP protein
60	277	21.2	246	14	AAW4761	Acetocetyl CoA re
61	276.5	21.2	249	23	ABP39980	Staphylococcus epi
62	275.5	21.1	272	22	AAU37095	Staphylococcus aur
63	275	21.1	285	22	AAW34648	E. coli cellular p
64	274.5	21.1	251	22	AAU34193	Staphylococcus aur
65	274.5	21.1	269	23	ABW82448	Heridically activ
66	274	21.0	206	23	AAW93345	Short-chain dehydr
67	273.5	21.0	254	22	AAW47522	(R)-2-oxotanol deny
68	273.5	21.0	286	22	AAU36267	Pseudomonas aerugi
69	273	20.9	202	23	AAU77210	Consensus protein
70	272.5	20.9	246	21	AAW15707	Staphylococcus aur
71	272.5	20.9	246	22	AAU33965	Staphylococcus aur
72	272.5	20.9	246	22	AAU36530	Staphylococcus aur
73	272.5	20.9	246	22	AAU37210	Staphylococcus aur
74	272.5	20.9	246	22	AAU37507	Staphylococcus aur
75	271.5	20.8	248	20	AAV69599	Chlamydia trachoma
76	270.5	20.7	267	21	AAW35505	Arabidopsis thalia
77	270.5	20.7	308	21	AAW35504	Arabidopsis thalia
78	269.5	20.7	242	22	AAW35381	Haemophilus influe
79	269	20.6	231	22	ABW39552	Staphylococcus epi
80	269	20.6	254	23	ABW48207	Listeria monocytog
81	268.5	20.6	246	22	AAW21155	S. aureus NADPH-de
82	268	20.6	186	19	AAW38474	S. pneumoniae 3-ox
83	267	20.5	247	16	AAW66291	Mycobacterium bovi

84 267 20.5 247 16 AAR63899 M. bovis PS5 ORP1
85 267 20.5 247 18 AAW40809 M. bovis PS5 opero
86 267 20.5 276 21 AAY54416 Secoisolaricresin
87 267 20.5 276 23 AAO21494 Secoisolaricresin
88 266.5 20.4 266 21 AAY92509 Human OXRE-6, Hom
89 266.5 20.4 268 16 ABB52552 Escherichia coli p
90 266.5 20.4 336 16 AAW06488 Malze TS2 sequence
91 265.5 20.4 252 23 AAO16940 Recombinant enzyme
92 265.5 20.4 273 21 AAY54414 Secoisolaricresin
93 264 20.2 261 13 AAR2756 NAD affinity gluc
94 262 20.1 272 21 AAB10740 B. megaterium gluc
95 262 20.1 277 21 AAY54413 Secoisolaricresin
96 262 20.1 340 21 AAB10741 H. ghallanli/B. me
97 261 20.0 243 23 ABB54107 Lactococcus lactis
98 260 19.9 253 23 AAO36249 Pseudomonas aerugi
99 259.5 19.9 258 23 ABB92143 Herbidicidally activ
100 258.5 19.8 158 23 ABB61039 Lactobacillus rham

ALIGNMENTS

RESULT 1
AAW71471
ID AAW71471 standard; Protein; 261 AA.

XX AAW71471:
16-DEC-1998 (first entry)

XX ERAB protein.

XX Endoplasmic reticulum associated amyloid-beta peptide binding protein;

KW ERAB protein; amyloid-beta peptide; inhibitor; demyelinating disease;

KW neurodegenerative disorder; therapy; Alzheimer's disease; schizophrenia;

KW Down's syndrome; Parkinson's disease; Huntington's disease;

XX Multiple sclerosis.

XX Homo sapiens.

XX WO9840484-A1.

XX 17-SEP-1998.

XX 12-MAR-1998; 98WO-US04915.

XX 12-MAR-1997; 97US-0815225.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Stern DM, Yan SD;

XX WPI; 1998-531524/45.

XX N-PSDB; AAV60576.

XX Endoplasmic reticulum associated amyloid-beta peptide binding

XX protein - inhibitors of which can be used to treat neurodegenerative

XX disorders

XX Claim 2; Fig 1D; 53pp; English.

XX This sequence is the endoplasmic reticulum associated amyloid-beta

XX peptide binding (ERAB) protein of the invention. The protein can be used

XX in a method for evaluating the ability of an agent to inhibit binding of

XX ERAB polypeptide to amyloid-beta peptide comprising: (a) incubating the

XX conditions; (b) determining the amount of amyloid-beta peptide bound to

XX ERAB polypeptide; (c) comparison of the amount of binding with results

XX from a control using no agent, so determining inhibition ability of the

XX agent. The inhibitors identified by the method can be used to treat a

XX neurodegenerative condition by administration of an agent that inhibits

XX binding of an ERAB polypeptide to amyloid-beta peptide, particularly

XX where the disease is Alzheimer's disease, Down's syndrome, Parkinson's

CC disease, Huntington's disease, schizophrenia, a demyelinating disease, or
CC multiple sclerosis. The inhibitors can also be used to treat other
CC neurodegenerative conditions including those associated with ageing,
CC dentatorubral and pallidolysian atrophy, Machado-Joseph disease,
CC muscular dystrophy, senility, spinocerebellar ataxia type I, spinobulbar
CC muscular atrophy, stroke, and trauma.
XX
SQ Sequence 261 AA;

Query Match 99.6%; Score 1299; DB 19; Length 261;
Best Local Similarity 99.6%; Pred. No. 1,4e-118;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAACRSYKGLVAVITGASGLATATRLVGGASAVLLDLPNSGGEAOKKGNVCV 60
1 MAACRSYKGLVAVITGASGLATATRLVGGASAVLLDLPNSGGEAOKKGNVCV 60
DB 1 MAACRSYKGLVAVITGASGLATATRLVGGASAVLLDLPNSGGEAOKKGNVCV 60
QY 61 APADVTSEKDYQTALALAKKFGKRVDAVANCAGIAVASKTYNLEKGGTHLEDFORVLDV 120
61 APADVTSEKDYQTALALAKKFGKRVDAVANCAGIAVASKTYNLEKGGTHLEDFORVLDV 120
DB 61 APADVTSEKDYQTALALAKKFGKRVDAVANCAGIAVASKTYNLEKGGTHLEDFORVLDV 120

QY 121 NLMGTENVIRLVAGEMGNEDPGGGRVITNTASVAFEGVQQAAYSASKGIYGMTL 180
121 NLMGTENVIRLVAGEMGNEDPGGGRVITNTASVAFEGVQQAAYSASKGIYGMTL 180
DB 121 NLMGTENVIRLVAGEMGNEDPGGGRVITNTASVAFEGVQQAAYSASKGIYGMTL 180

QY 181 PIARDLAPIGIRVMTIAPGLFPTPLTSLPEKVSNTLASQVFPSPRLGDPAEYAHVQAI 240
181 PIARDLAPIGIRVMTIAPGLFPTPLTSLPEKVSNTLASQVFPSPRLGDPAEYAHVQAI 240
DB 181 PIARDLAPIGIRVMTIAPGLFPTPLTSLPEKVSNTLASQVFPSPRLGDPAEYAHVQAI 240

QY 241 IENPFLNGEVIRLDGAIKMQP 261
241 IENPFLNGEVIRLDGAIKMQP 261
DB 241 IENPFLNGEVIRLDGAIKMQP 261

RESULT 2
AAV32239
ID AAV32239 standard; Protein; 260 AA.
XX AAV32239;
XX 15-FEB-2000 (first entry)

XX Alzheimer-associated beta-amyloid binding protein (ERAB).
XX
XX Alzheimer-associated beta-amyloid binding protein; ERAB; mouse;
XX Leydig cell; differential display RT-PCR; DDRT-PCR;
XX short chain alcohol dehydrogenase; SCAD; testis; marker;
XX spermatogenesis.
XX
XX Mus musculus.

OS Mus musculus.
XX
XX Location/Qualifiers
FH 10..15
FT Region
FT /note= "beta sheet region A"
FT 18..32
FT Region
FT /note= "alpha helix region A"
FT 35..41
FT Region
FT /note= "beta sheet region B"
FT 43..57
FT Region
FT /note= "alpha helix region B"
FT 61..66
FT Region
FT /note= "beta sheet region C"
FT 70..80
FT Region
FT /note= "alpha helix region C"
FT 84..94
FT Region
FT /note= "beta sheet region D"
FT 109..133
FT Region
FT /note= "alpha helix region D"
FT 143..153
FT Region
FT /note= "beta sheet region E"
FT 167..171
FT Region
FT /note= "SCAD motif"
FT 185..186


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FT      /note= "alpha helix region A"
FT      190..196
FT      Region
FT      /note= "beta sheet region F"
FT      204..218
FT      Region
FT      /note= "alpha helix region F"
FT      247..252
FT      Region
FT      /note= "beta sheet region G"
XX      WO954347-A2.
XX      28-OCT-1999.
XX      19-APR-1999; 99WO-EP02610.
XX      17-APR-1998; 98US-0082257.
XX      (HORM-) INST HORMON & FORPFLANZUNGSPORSCHUNG GM.
XX      Iwell R, Spiess A, Balvers M, Jaehner D, Hansis C;
XX      WPI: 2000-052699/04.
XX      N-PSDB: AA234663.
XX      Novel differential display reverse transcription PCR method used to
XX      detect genes expressed in mutant tissues
XX      Claim 4; Fig 2; 40pp; English.
XX      This sequence represents murine Alzheimer-associated beta-amyloid
XX      binding protein (ERAB, see AY32239), a novel member of the SCAD
XX      (short chain alcohol dehydrogenase) family of steroid metabolising
XX      and related enzymes. The sequence was deduced from cDNA (see
XX      AA234663) identified using a novel differential display RT-PCR method
XX      for analysis of w/wv mouse testis gene products. ERAB is
XX      specifically upregulated in the testicular Leydig cells of w/wv
XX      azoospermic mutant mice, suggesting an important role in the
XX      establishment and support of spermatogenesis. The invention also
XX      relates to vectors, host cells, methods for expressing the ERAB
XX      nucleic acid, and antibodies. The nucleic acid and protein are
XX      useful e.g. as markers for testicular development.
XX      SQ      Sequence      260 AA:

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Query Match      87.9%; Score 1146; DB 21; Length 260;
Best Local Similarity 87.6%; Pred. No. 1,2e-103;
Matches 226; Conservative 18; Mismatches 14; Indels 0; Gaps 0;

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OY      4 ACRSVKGLVAVITGASGIGLATAERLVGOGASAVLDDLPSNGGEAOKKIGNNCFAPA 63
OY      3 AVRSYKGLVAVITGASGIGLATAERLVGOGATAVLDPSEGEAOKKIGESCFAPA 62
OY      64 DVTSEKDVOTALALAKKFGKRVDAVNCAGIYASAKTYNLKGCQHTLEDFQRYADVNL 123
OY      63 NTSSEKIOALTLAKKFKRQIDAVNCAGINVAIKTHOKNKHITLEDQRYAVNL 122
OY      124 GFENVIRLVAGEMGONEPDGQGRVINTASVAAPEGOVGAAYASAKSGIVGKTLPIA 183
OY      123 GFENVIRLVAGEMGONEPDGQGRVINTASVAAPEGOVGAAYASAKSGIVGKTLPIA 182
OY      184 RDLAPGIRVMTIAPGLFGTPLLTSIPKVSNFLASOVFPFRLDGPAYAHLYOATLEN 243
OY      183 RDLAPGIRVMTIAPGLFGTPLLTSIPKVSNFLASOVFPFRLDGPAYAHLYOATLEN 242
OY      244 PFLNGEIVIRLDGAIRMP 261
OY      243 PFLNGEIVIRLDGAIRMP 260

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RESULT 3
AAM67934
ID      AAM67934 standard; Protein; 227 AA.
XX
AC      AAM67934;

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XX      25-MAR-1999 (first entry)
XX      Fragment of human secreted protein encoded by gene 8.
XX      Human; secreted protein; fusion protein; gene therapy; protein therapy;
XX      diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
XX      developmental abnormality; foetal deficiency; blood; allergy; renal;
XX      immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
XX      inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;
XX      cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
XX      osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
XX      endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX      Homo sapiens.
XX      WO9842738-A1.
XX      01-OCT-1998.
XX      19-MAR-1998; 98WO-US05311.
XX      30-MAY-1997; 97US-0050937.
XX      21-MAR-1997; 97US-0041276.
XX      21-MAR-1997; 97US-0041277.
XX      21-MAR-1997; 97US-0041281.
XX      21-MAR-1997; 97US-0042344.
XX      30-MAY-1997; 97US-0048069.
XX      30-MAY-1997; 97US-0048094.
XX      30-MAY-1997; 97US-0048095.
XX      30-MAY-1997; 97US-0048096.
XX      30-MAY-1997; 97US-0048099.
XX      30-MAY-1997; 97US-0048131.
XX      30-MAY-1997; 97US-0048135.
XX      30-MAY-1997; 97US-0048154.
XX      30-MAY-1997; 97US-0048160.
XX      30-MAY-1997; 97US-0048186.
XX      30-MAY-1997; 97US-0048187.
XX      30-MAY-1997; 97US-0048188.
XX      30-MAY-1997; 97US-0048350.
XX      30-MAY-1997; 97US-0048351.
XX      30-MAY-1997; 97US-0048352.
XX      30-MAY-1997; 97US-0048355.
XX      05-AUG-1997; 97US-0054804.
XX      (HUMA-) HUMAN GENOME SCI INC.
XX      Brewer LA, Duan R, Ebner R, Ferris AM, Florence KA,
XX      Greene JM, Hu JS, Latleier DW, Moore PA, NI J, Olsen HS;
XX      Rosen CA, Ruben SM, Shi Y, Young P;
XX      WPI: 1999-070066/06.
XX      N-PSDB: AAX00618.
XX      New isolated human genes and the secreted polypeptides they encode -
XX      useful for diagnosis and treatment of e.g. cancers, neurological
XX      disorders, immune diseases, inflammation or blood disorders
XX      Disclousure; Page 11; 385pp; English.
XX      This sequence represents a fragment of a secreted human protein encoded
XX      by the nucleic acid molecule detailed in the descriptor line. The gene
XX      can be used to generate fusion proteins by linking to the gene to a
XX      human immunoglobulin Fc portion (e.g. AAX00602) for increasing the
XX      stability of the fused protein as compared to the human protein only.
XX      The invention relates to 87 novel genes and their fragments (nucleic
XX      acid sequences: AAX00611-X00724; amino acid sequences AAM67807-W68004)
XX      which are useful for preventing, treating or ameliorating medical
XX      conditions e.g. by protein or gene therapy. Also, pathological
XX      conditions can be diagnosed by determining the amount of mutations in
XX      polypeptides in a sample or by determining the presence of mutations in
XX      the new polynucleotides. Specific uses are described for each of the 87
XX      polynucleotides, based on which tissues they are most highly expressed in

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CC (see AAX00611 for described uses).

XX Sequence 227 AA;

Query Match 87.1%; Score 1136; DB 20; Length 227;
Best Local Similarity 99.6%; Pred. No. 9,7e-103;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 35 ASAYLDDLPSNGSGAOKKIGNNVCVPADVTSEKDVQIALAKKFGGVDAVNCAGI 94
DB 1 ASAYLDDLPSNGSGAOKKIGNNVCVPADVTSEKDVQIALAKKFGGVDAVNCAGI 60
QY 95 AVASKTYNLKKGQHTLEDFQRLVDVNLKMGTFNIRLVAGEMGNRPDGGGQGVIIINTA 154
DB 61 AVASKTYNLKKGQHTLEDFQRLVDVNLKMGTFNIRLVAGEMGNRPDGGGQGVIIINTA 120
QY 155 SVAAPEGVGCAAVSASKGIVGKTLPIARDLPIGIRVMTIAPGLFGLTSLPEKVS 214
DB 121 SVAAPEGVGCAAVSASKGIVGKTLPIARDLPIGIRVMTIAPGLFGLTSLPEKVS 180
QY 215 NFLASOYFPPSRIDGPAEYAHLYQAIIENPFLNGEVIRLDGAIKMP 261
DB 181 NFLASOYFPPSRIDGPAEYAHLYQAIIENPFLNGEVIRLDGAIKMP 227

RESULT 4

ABB62988 ID ABB62988 standard; Protein: 255 AA.

XX ABB62988;

DT 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 15756.

XX Drosophila; developmental biology; cell signalling; insecticide;

XX pharmaceutical.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

XX 11-JUL-2000; 2000US-0614150.

XX (PERE) PE CORP NY.

XX Venter JC, Adams M, Li FWD, Myers EW;

XX WPI; 2001-656860/75.

XX N-PSDB; ABL07091.

XX New isolated nucleic acid detection reagent for detecting 1000 or more

XX genes from Drosophila and for elucidating cell signalling and cell-cell

XX interactions -

XX Disclosure: SEQ ID NO 15756; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent

XX capable of detecting 1000 or more genes from Drosophila. The invention is

XX useful in developmental biology and in elucidating cell signalling and

XX cell-cell interactions in higher eukaryotes for the development of

XX insecticides, therapeutics and pharmaceutical drugs. The invention

XX discloses genomic DNA sequences (ABLI6176-ABLI30511), expressed DNA

XX sequences (ABLI01840-ABLI6175) and the encoded proteins

XX (ABBS7737-ABBS7072).

XX The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 255 AA;

Query Match 69.8%; Score 910; DB 22; Length 255;
Best Local Similarity 68.9%; Pred. No. 1.3e-80;
Matches 175; Conservative 29; Mismatches 50; Indels 0; Gaps 0;

QY 8 VAGIYAVITGGASGLGNAERLVQGSAAVLDD:PNNGGGAOKKIGNNVCVPADVTSE 67
DB 2 INNAVSLVVGASGLGNAERLVQGSAAVLDD:PNNGGGAOKKIGNNVCVPADVTSE 61
QY 68 EKDVSALQTDANKFGRDLTVNCAGTATAVTFNKNVAHRLDFQRLVINTVGFEN 127
DB 62 EKDVSALQTDANKFGRDLTVNCAGTATAVTFNKNVAHRLDFQRLVINTVGFEN 121
QY 128 VIRLVAGEMGNRPDGGGQGVIIINTASVAAPEGVGCAAVSASKGIVGKTLPIARDL 187
DB 122 VIRLVAGEMGNRPDGGGQGVIIINTASVAAPEGVGCAAVSASKGIVGKTLPIARDL 181
QY 188 PIGIRVMTIAPGLFGLTSLPEKVSNFLASOYFPPSRIDGPAEYAHLYQAIIENPFLN 247
DB 182 TGGIRCTIAPGLFGLTSLPEKVSNFLASOYFPPSRIDGPAEYAHLYQAIIENPFLN 241
QY 248 GEVIRLDGAIKMP 261
DB 242 GEVIRLDGAIKMP 255

RESULT 5

AAW06513 ID AAW06513 standard; Protein: 388 AA.

XX AAW06513;

DT 08-MAR-1997 (first entry)

XX Flavobacterium ORF-5 gene product.

XX Carotenoid; lycopene; beta-carotene; echinenone; cantaxanthin;

XX zeaxanthin; adonixanthin; astaxanthin.

XX Flavobacterium sp. R1534 WT (ATCC 21588).

XX EP747483-A2.

XX 11-DEC-1996.

XX 29-MAY-1996; 96EP-0108556.

XX 09-JUN-1995; 95EP-0108888.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Hoffmann H, Pasamontes L, Tessier M, Van Loon A;

XX WPI; 1997-023160/03.

XX N-PSDB; AAT45143.

XX Flavobacterium gene sequences encoding carotenoid biosynthesis

XX enzymes - for the production of carotenoid(s), useful in foods and

XX animal feeds

XX Example 2; Fig 7; 80pp; English.

XX A polypeptide (AAW06513) showing approx. 30% homology to

XX streptomyces polyketide synthases was identified as the product

XX of ORF-5 from a carotenoid gene cluster (see also AAT45143) of

XX Flavobacterium sp. R1534. 5 Other open reading frames of the

XX gene cluster coded for carotenoid biosynthetic enzymes (see also

XX AAW06515-18 and AAW06571) and can be used to produce carotenoids in

XX transformed host cells.

XX Sequence 388 AA;

FR	13-DEC-1996;	96US-0036281.
XX	(ELIL) LILLY & CO ELI.	
XX		
XX	Baltz RH, Burgett SG, Dehoff BS, Hoskins JR, Jaskunas SR;	
XX	Mills BJ, Norris FH, Peery RB, Rocky PK, Rostock PR;	
XX	Sketard PJ, Smith MC, Solenberg PJ, Treadway PJ;	
XX	Young Bellido ML;	
XX	WPI, 1998-348529/30.	
XX		
XX	Streptococcus pneumoniae nucleic acid sequences - used in DNA chips	
XX	for evaluating gene expression, and identification of virulence	
XX	genes	
XX	Claim 3; Page 270; 333pp; English.	
XX		
XX	This sequence represents a S. pneumoniae fatty acid biosynthesis	
XX	protein. The invention provides DNA sequences (AAV65201 to AAV65304)	
XX	from the Streptococcus pneumoniae genome and corresponding protein	
XX	sequences (AAW80005 to AAW80728). The protein sequences are classified as	
XX	hypothetical, cell wall biosynthetic, external target, or minimal gene	
XX	set proteins. A recombinant host containing a vector comprising any of	
XX	the above nucleic acids can be used for the recombinant expression of the	
XX	proteins. The invention also provides a DNA chip having arrayed on it at	
XX	least 15 base pair fragment of any one or more of these DNA sequences.	
XX	The DNA chip can be used methods for evaluating gene expression in S.	
XX	pneumoniae and for identifying virulence genes in S. pneumoniae.	
XX	Antibodies that selectively bind to the above proteins or peptide	
XX	fragments can be used to treat S. pneumoniae infection. The antibodies	
XX	can also be used to detect S. pneumoniae cells.	
XX		
XX	Sequence 243 AA;	
XX		
XX	Query Match 25.3%; Score 329.5; DB 19; Length 243;	
XX	Best Local Similarity 35.1%; Pred. No. 6, 1e-24;	
XX	Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;	
QY	15 ITGASGIGLTAETPELVGQASAVLIDIPNSGG-----AQAKLGNKCYFAPADYSE 68	
DB	10 ITGSSRGIGLTAHFFAQAQANITY---NSRGAISEELLAEFSNYGKVPISQVDF 65	
QY	69 KDVGAFALAKKGFEGVDVAVACIQAASKTYNLRKGFHTLEDPCFVLDVNLNGTEV 128	
DB	66 ADARKMIDQALAEIGSDVVLVNNAI--TQDTLMKKM---TEADFERKVLNLGAFNM 119	
QY	129 IRLVAGEGONPEDDGGGRGVYIINTASVAAPFGQVQAANSKSGITGMILPTIRDLAP 188	
DB	120 TQSVL-----KPKMKAREGAIINNSVAVGLMGNQANYPASKRGLIGFTKSVAREVAS 173	
QY	189 IGRVMTAPLGFGLPTLTSLPEKSNFLASGVPPSPRLGPAEYAHLVQAIINPFLNG 248	
DB	174 RHIRRVNVAIPGIEEDMTALLSDRKKEATLQIPM-KFEGQAEQVADLTVFLAGQDYLTG 232	
QY	249 EYIRLDGAIIPM 259	
DB	233 QVIAIDGGLSM 243	
RESULT 9		
ID	AAAB15706 standard; Protein; 243 AA.	
XX	AAAB15706;	
XX	07-DEC-2000 (first entry)	
XX	Streptococcus pneumoniae FabG polypeptide.	
XX	Streptococcus pneumoniae; FabG; 3-oxoacyl-acyl carrier protein reductase;	
XX	antibacterial; cytosolic; antituberc; cancer; gastric ulcer; gastritis;	
XX	Helicobacter pylori infection; microbial infection.	

XX Streptococcus pneumoniae.
 OS
 XX WO200044885-A1.
 XX
 XX 03-AUG-2000.
 XX
 XX 19-JAN-2000; 2000WO-US01131.
 XX
 XX 27-JAN-1999; 99US-0239052.
 XX
 XX (SMIX) SMITHKLINE BEECHAM CORP.
 XX
 XX Holmes DJ, Mooney J, Zhong YY, Debouck C, Jaworski DD, Wang M;
 PI Warren RL, Kosmatka AL, Mcdevitt D, Ingraham KA, Chalker AF;
 PI So CY, Wallis NG, Pearson SC;
 XX
 XX WPI, 2000-482971/42.
 XX N-PSDB; AAA/4684.
 DR
 XX FabG polypeptide, isolated from streptococcus pneumoniae, is used to
 PT treat microbial diseases, identify agonists and antagonists for
 PT treating microbial infections and to detect diseases associated with
 PT microbial infections -
 PS
 XX Claim 1; Page 3; 40pp; English.
 XX
 CC The present sequence is a FabG (2-oxoacyl-acyl carrier protein
 CC reductase) polypeptide. A full length FabG gene was isolated from a
 CC Streptococcus pneumoniae 0100993 DNA library in E. coli. FabG
 CC polynucleotides and polypeptides are used for detection and treatment of
 CC microbial diseases. They may also be used to identify antagonists and
 CC agonists which can then be used to treat microbial diseases. Compounds
 CC that interfere with the initial physical interaction between a pathogen
 CC and a host have been identified. The compounds are able to prevent the
 CC adhesion of bacteria to mammalian extracellular proteins in wounds,
 CC prevent adhesion between mammalian extracellular proteins and bacterial
 CC FabG proteins which mediate tissue damage and/or to block normal
 CC progression of pathogenesis in infections mediated by implantation of
 CC in-dwelling devices or other surgical techniques. The FabG
 CC polypeptides, polynucleotides, antagonists and agonists are especially
 CC useful in the treatment of Helicobacter pylori infection. They may be
 CC used to decrease H. pylori-induced cancers and to prevent, inhibit
 CC and/or cure gastric ulcers and gastritis.
 CC
 XX
 XX Sequence 243 AA;
 SQ
 Query Match 25.3%; Score 329.5; DB 21; Length 243;
 Best Local Similarity 35.1%; Pred. No. 6.1e-24;
 Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;

AAU37767
 ID AU37767 standard; Protein; 243 AA.
 XX
 XX AC AU37767;
 XX
 XX 14-FEB-2002 (first entry)
 XX
 XX Streptococcus pneumoniae cellular proliferation protein #196.
 DE
 XX Antisense: prokaryotic cellular proliferation protein;
 XX antibiotic; antibacterial; drug design.
 KW
 XX Streptococcus pneumoniae.
 OS
 XX WO200170955-A2.
 XX
 XX 27-SEP-2001.
 XX
 XX 21-MAR-2001; 2001WO-US09180.
 XX
 XX 21-MAR-2000; 2000US-191078P.
 XX 23-MAY-2000; 2000US-206848P.
 XX 26-MAY-2000; 2000US-207127P.
 XX 23-OCT-2000; 2000US-242578P.
 XX 27-NOV-2000; 2000US-253625P.
 XX 22-DEC-2000; 2000US-257931P.
 XX 16-FEB-2001; 2001US-269308P.
 XX
 XX (ELITRA) ELITRA PHARM INC.
 XX
 XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX
 XX WPI; 2001-611495/70.
 DR N-PSDB; AAS55626.
 DR
 XX New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 PT
 XX
 XX Example 3; Seq ID No 13360; 511pp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
 CC pneumoniae, pseudomonas aeruginosa and Enterococcus faecalis. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: the sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pot_sequences.
 XX
 XX Sequence 243 AA;
 SQ
 Query Match 25.3%; Score 329.5; DB 22; Length 243;
 Best Local Similarity 35.1%; Pred. No. 6.1e-24;
 Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;

Db 66 ADAKRMIDQALAEISVDVLYNNAGI--TQDTLMKMK-----TEADFEKVLKYNLTGAFNM 119
 QY 129 IRLVAGENGQNEPDGQGRGVYIINTASVAFEGVGQAAYSASKGIVGMLPIARDLAP 188
 Db 120 TQSVL-----KPMKAKREGAIIMSSVYGLMGNIGQANYAASAKGLIGFTKSVAREVAS 173
 QY 189 IGIRVMTAPGLFGFTPLTSLPEKVSNFLASQVFPSPRLGDPAPAEYAHLYQAIIENPFLNG 248
 Db 174 RNIRNVYIAPGKMTIESDMTRAILSDKIKENTLAQIRM-KERQGAEGVADLTIVFLAGQDYLTG 232
 QY 249 EVIRLDGAIRM 259
 Db 233 QVIAIDGGLSM 243
 RESULT 11
 AAU37988 standard; Protein; 243 AA.
 AC AAU37988;
 XX 14-FEB-2002 (first entry)
 DT Streptococcus pneumoniae cellular proliferation protein #417.
 DE Streptococcus pneumoniae cellular proliferation protein #417.
 XX Antisense; prokaryotic cellular proliferation protein;
 KM antibiotic; antibacterial; drug design.
 XX Streptococcus pneumoniae.
 OS
 XX MO200170955-A2.
 PN 27-SEP-2001.
 PD 21-MAR-2001; 2001MO-US09180.
 PF 21-MAR-2000; 2000US-191078P.
 PR 23-MAY-2000; 2000US-206848P.
 XX 26-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242378P.
 XX 27-NOV-2000; 2000US-253623P.
 PR 22-DEC-2000; 2000US-257931P.
 XX 16-FEB-2001; 2001US-269308P.
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 PI WPI; 2001-611495/70.
 DR N-PSDB; AAS55847.
 XX
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 XX
 PS Example 3; Seq ID No 13581; 511bp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC Escherichia coli, Staphylococcus aureus, Enterococcus faecalis. The
 CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp://ipo.int/pub/published_pct_sequences.
 CC
 SC Sequence 243 AA;
 Query Match 25.3%; Score 329.5; DB 22; Length 243;
 Best Local Similarity 35.1%; Pred. No. 6.1e-24;
 Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;
 QY 15 ITGASGIGLATPARELYGQASAVLLDPNSGGE-----AQAKKLNCCVFPADYTS 68
 Db 10 ITGSRGIGLAIARKEFAQAGANIYL---NSRGAISELLAEFSNVIKYPVTSQDVSD 65
 QY 69 KDVOATALAKGFGFVDVAVNCAGIIVASKTYNLKKGQHTLEDFOVLVDVNLMTGFNV 128
 Db 66 ADAKRMIDQALAEISVDVLYNNAGI--TQDTLMKMK-----TEADFEKVLKYNLTGAFNM 119
 QY 129 IRLVAGENGQNEPDGQGRGVYIINTASVAFEGVGQAAYSASKGIVGMLPIARDLAP 188
 Db 120 TQSVL-----KPMKAKREGAIIMSSVYGLMGNIGQANYAASAKGLIGFTKSVAREVAS 173
 QY 189 IGIRVMTAPGLFGFTPLTSLPEKVSNFLASQVFPSPRLGDPAPAEYAHLYQAIIENPFLNG 248
 Db 174 RNIRNVYIAPGKMTIESDMTRAILSDKIKENTLAQIRM-KERQGAEGVADLTIVFLAGQDYLTG 232
 QY 249 EVIRLDGAIRM 259
 Db 233 QVIAIDGGLSM 243
 RESULT 12
 AAM01032
 ID AAM01032 standard; Protein; 243 AA.
 XX
 AC AAM01032;
 XX 02-OCT-2001 (first entry)
 DT CFE 35 protein sequence.
 DE
 XX Antibacterial; vaccine; gene therapy; bacterial cell wall viability;
 KM CFE; CEG; Conserved Essential Gene; bacterial infection;
 KM antisense therapy; antibiotic resistance.
 OS
 XX Streptococcus pneumoniae.
 XX
 PI WO200149721-A2.
 PN 12-JUL-2001.
 PD 29-DEC-2000; 2000MO-US35604.
 PF 30-DEC-1999; 99US-0174089.
 XX
 PR (BRIN) BRISTOL-MYERS SQUIBB CO.
 PA
 PI Dougherty TJ, Pucci MJ, Dougherty BA, Davison DB, Bruccoleri RE;
 PI Thanassi JA;
 PI WPI; 2001-496721/54.
 DR N-PSDB; AAM90731.
 XX
 PT Nucleic acids encoding conserved essential genes involved in bacterial
 PT replication which are potential targets for the treatment of antibiotic
 PT resistant bacterial infections -
 XX
 PS Claim 27; Page 273; 380pp; English.
 XX
 CC The present invention relates to nucleic acids (AAM90701-AAM90918)
 CC encoding polypeptides (AAM01002-AAM01114), which are essential for the
 CC viability of prokaryotic cell wall. The acronym CFE stands for "Conserved
 CC Expression", where CEG stands for "Conserved Essential Gene". The nucleic

CC acids are useful for detecting the presence of proteins essential for the
CC viability of a bacterial cell wall in samples such as cells, tissues,
CC biological fluids, blood, serum, nose, ear or throat swabs with ligands,
CC and for detecting corresponding target nucleic acid molecules with
CC complementary sequences. The nucleic acids are also useful for
CC determining whether a genomic nucleotide sequence of interest is
CC essential for viability of a bacterial cell or whether it resides within
CC an operon, by integrating an exogenous nucleotide sequence comprising a
CC portion of an open reading frame of the genomic sequence of interest
CC (comprising 200-500 base pairs) into the genomic sequence of interest
CC which confers a selectable phenotype to the cell, and determining cell
CC viability with a selection agent such as chloramphenicol. The nucleic
CC acids and proteins are also useful as vaccines and for treating bacterial
CC infections with gene therapy and antisense therapy. The nucleic acids
CC also enable identification of targets suitable for the treatment of
CC antibiotic resistant bacterial infections.

XX Sequence 243 AA;

Query Match 25.2%; Score 328.5; DB 22; Length 243;
Best Local Similarity 34.7%; Pred. No. 7.7e-24;
Matches 87; Conservative 37; Mismatches 104; Indels 23; Gaps 6;

QY 15 ITGASGLATAEPLVCGASAVLLDLPNSGGE-----AQAKKLNVCYPADAVTSE 68
DB 10 ITGSSRGIGLAIHKEFAQGANIVL-----NSRGAISEELAEFSNYGIRKVPISGDVSD 65
QY 69 KDVQALALAKGKFGFVDVAVNCAGIAVASKTYNKKQGTHTLEDFORVLDVNLGTFNV 128
DB 66 ADARKKIDQALIELSVLVNNAI--TQDTLMKK-----TEADFEYLVNLTGARNM 119
QY 129 IELVAGMGQNEPDGQGGGVITINNVAAFEFGVQGAAYSASKSGIYMTLPARDIAP 188
DB 120 TQSVL-----KPMKAREGAIINMSVYGLMNGINQANVASKAGLIGFTKSVAREVAS 173
QY 189 IGRVWTAPGLFGPTLTLSPKYSNPLASQVPPSRLDPAEYAHVQAITTEPFLNG 248
DB 174 RIRRVNVIAFGMIESMTAILSDKIKKATLQIIP-KERGAQVADLTVPFLAGDYLTG 232
QY 249 EVIRLDGATRM 259
DB 233 QVAIDGGLSM 243

RESULT 13

ID ABB54087 standard; Protein; 243 AA.

XX ABB54087;

XX 16-MAY-2002 (first entry)

XX Lactococcus lactis protein dabG1.

XX Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese;

XX Lactococcus lactis IL1403.

XX OS FR2807446-A1.

XX PD 12-OCT-2001.

XX PF 11-APR-2000; 2000FR-0004630.

XX PR 11-APR-2000; 2000FR-0004630.

XX PA (INRG) INRA INST NAT RECH AGRONOMIQUE.

XX PI Bolotine A, Sorokine A, Renault P, Ehrlich SD;

XX DR WPI; 2002-043418/06.

XX PT New nucleotide sequence useful in the identification of Lactococcus

PT Lactis and related species -
XX
PS Claim 6; SEQ ID No 789; 2504pp; French.

XX The present invention is related to a Lactococcus lactis nucleotide
CC sequence (AB90521) and related proteins (ABB53300-ABB55621). The
CC nucleic acid sequence is useful in the detection and/or amplification of
CC nucleic acid sequence, particularly to identify Lactococcus lactis or
CC related species. The proteins of the invention are useful for the
CC biosynthesis or biodegradation of a composition of interest. The
CC invention helps research in lactic bacteria, particularly useful in the
CC production of yogurt and cheese.
CC Note: The sequence data for this patent is based on equivalent patent
CC WO2001/77334 (published 18-Oct-2001) which is available in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 243 AA;

Query Match 25.1%; Score 327.5; DB 23; Length 243;
Best Local Similarity 31.7%; Pred. No. 9.6e-24;
Matches 82; Conservative 48; Mismatches 104; Indels 25; Gaps 6;

QY 8 VKGLVAVITGASGLATAEPLVCGASAVLLDLPNSGGEAAAKL-----GNVCVF 60
DB 3 IKKNVTFVGTSTRIGIAIALQFAKASNLII-----NGRSASEELAEFTYGVKAVG 57
QY 61 APADVTESEKDVQALALAKGKFGFVDVAVNCAGIAVASKTYNKKQGTHTLEDFORVLDV 120
DB 58 ISGSIKSEDAKQVAAIETLSVDLVNNAI--TRDGLSKMSB---EDPESVLKI 111
QY 121 NMGTFVAVIRLVAGMGQNEPDGQGGGVITINNVAAFEFGVQGAAYSASKSGIYMTLP 180
DB 112 NLTAFAFMNTQAVL-----KPMTRARGAIINISVYGLMNGINQANVASKAGLIGLTR 165
QY 181 PIARDLAPIGIRVWTAPGLFGPTLTLSPKYSNPLASQVPPSRLDPAEYAHVQAITTEPFL 240
DB 166 SIAREVAAARNRVAAVAPGFIESDMEVLDKXVADAKKQIIP-KRGMDEIATATQFL 224
QY 241 IENPFLNGEVIRLDGATRM 259
DB 225 AEQRYMTGOVLTIDGVSVM 243

RESULT 14

ID AAU35328 standard; Protein; 245 AA.

XX AAU35328;

XX 14-FEB-2002 (first entry)

XX Enterococcus faecalis cellular proliferation protein #615.

XX Antisense; prokaryotic cellular proliferation protein;

XX antibiotic; antibacterial; drug design.

XX Enterococcus faecalis.

XX OS WO200170955-A2.

XX PD 27-SEP-2001.

XX PF 21-MAR-2001; 2001WO-US09180.

XX PR 21-MAR-2000; 2000US-191078P.

XX PR 23-MAY-2000; 2000US-206848P.

XX PR 26-MAY-2000; 2000US-207727P.

XX PR 23-OCT-2000; 2000US-242578P.

XX PR 27-NOV-2000; 2000US-253625P.

XX PR 22-DEC-2000; 2000US-257931P.

XX PR 16-FEB-2001; 2001US-269308P.

XX PA (ELT-) ELITRA PHARM INC.

XX Haselbeck R, Ohlsen KL, Zyskind JM, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX WPI, 2001-611495/70.
 DR N-PSDB; AAS53187.
 XX New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 XX
 PS Example 3; Seq ID No 10921; 51bp; English.
 XX The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
 CC pneumoniae, pseudomonas aeruginosa and *Enterococcus faecalis*. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pcr_sequences.
 XX Sequence 245 AA;
 SQ
 Query Match 24.7%; Score 321.5; DB 22; Length 245;
 Best Local Similarity 33.7%; Pred. No. 3.8e-23;
 Matches 84; Conservative 38; Mismatches 108; Indels 19; Gaps 5;
 QY 15 ITGGASGLGATFARLIVGASAVLTD---LPSNGGEAOKKLGNCVPAPADVSEKD 70
 DB 10 ITGSTRGIGKAVLAFAKESANITLNGRSETTPQRQREIA--FGVACIGSDISPDFA 67
 QY 71 VQTALAIARAKRGFADVAVNCAGIAVASKYTNLKKGGTHLEDFQVRLDVNLMGTENVIR 130
 DB 68 AGEMIQATVDTQISDILVNNAGIT-----NDKLLRMTEDEPNACIDILVGTFFMTQ 121
 QY 131 LVAGMGONEPDQGGRGVITNTASVAFSEGVQAAVSAKSGIVGMTLPIARDLPIG 190
 DB 122 QAVKRMKQ-----RSGRITMASVSGLMGNVQDANTAAKAGVGTTSVAKEVAPRG 175
 QY 191 IRVMTIAGLEGTPLTSLPERKVSNTLASQVPPFSRUGDPAEYAHVQVATIENTPFLNGEV 250
 DB 176 ITCNAIAGFQIETEXTVLSKRVKTQMAQIPLOT-FQGVEDVAATATFLAKSPYITGVGV 234
 QY 251 IRLDGAIRM 259
 DB 235 VAVDGGGLVAV 243
 RESULT 15
 AAU28344
 ID AAU28344 standard; Protein; 257 AA.
 XX AAU28344;
 AC 18-DEC-2001 (first entry)
 DT Novel human secretory protein, Seq ID No 701.
 XX
 KW Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KW ischaemia reperfusion injury; haematopoiesis; cancer; neuropathy;
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;

KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;
 KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 KW fertility; analgesic; pain; antigen.
 OS Homo sapiens.
 XX
 PN WO200166689-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 05-MAR-2001; 2001MO-US04942.
 XX
 PR 07-MAR-2000; 2000US-0519705.
 PR 19-MAY-2000; 2000US-0574454.
 PR 17-JUN-2000; 2000US-0596193.
 PR 14-JUL-2000; 2000US-0616847.
 PR 19-SEP-2000; 2000US-065363.
 PR 20-OCT-2000; 2000US-0693267.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
 PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
 XX WPI, 2001-589934/56.
 DR N-PSDB; AAS43244.
 DR Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders -
 XX
 PS Example 2; SEQ ID No 701; 107bp; English.
 XX The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing haematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I), (II) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions,
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
 CC analgesic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAU28020-AAU28395 represent novel human secreted protein
 XX amino acid sequences of the invention.
 SQ Sequence 257 AA;
 XX
 Query Match 24.3%; Score 317; DB 22; Length 257;
 Best Local Similarity 31.5%; Pred. No. 1.1e-22;


```

Matches      82;  Conservative      42;  Mismatches      110;  Indels      26;  Gaps      5;

QY          5  CRSVGLVAVITGASGLATAERLVGGASAVLLDPPNSGGEQAARKIGNCVFAPAD 64
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB          17  CDSEMDKCAVGVGSGRGIGRAVAQQLMARGYRLAVIARNEGAKAAADLGSDHIAFSCD 76
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY          65  VISESDVQATALAKGKGRVAVNACGI-----AVASKYNNLKKGTHTLEDQRVID 119
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB          77  VAKEDHVQNTFEEMEKHGKRVNPLVNAAGINRFDGLLVKTKT-----EDMVSQLH 125
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY          120  VLMGTFNVRIVAGEMQNEPDQGGQGVIIINTASVAAFEGVQQAAYSASKGIVGMT 179
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB          126  TNLGSMETCKKAMRTMIQ-----QGGSIVNVSIVGLKNGSGQSYSAKSGIVGFS 179
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY          180  LPIARDLAFIGRVKTIARGLGTPLTSLPKVSNFLASQVFPFSRIGDPAEVAHLVQA 239
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB          180  RALAKEVARKKIRVNVAPGVYHTDKTKLEE---HLKKNIPL-GREGETIEVAHAYVF 235
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY          240  IIEPPLNGEVIRLDGAIRM 259
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB          236  LLESPIYTHVLVVDGLOL 255
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

RESULT 16
AAMS0255
ID AAMS0255 standard; Protein; 237 AA.

XX AAMS0255;

DT 21-JAN-2002 (first entry)

DE Human dehydrogenase 21509.

KM Dehydrogenase; human; ovarian cancer; colon cancer; lung cancer;
KM liver cancer; metastasis; antitumor; therapy; diagnosis.

OS Homo sapiens.

FX Homo sapiens

FX Key Location/Qualifiers
3..229
Domain /note="short-chain alcohol dehydrogenase domain"
148..158
Region /note="short-chain alcohol dehydrogenase family
signature"

FT Modified-site 114..116
FT /note="O-phosphorylated by protein kinase C"
FT Modified-site 66..69
FT /note="O-phosphorylated by casein kinase II"
FT Modified-site 95..98
FT /note="O-phosphorylated by casein kinase II"
FT Modified-site 9..14
FT /note="N-myristoylated"
FT Modified-site 38..43
FT /note="N-myristoylated"
FT Modified-site 110..115
FT /note="N-myristoylated"
FT Modified-site 128..133
FT /note="N-myristoylated"
FT Modified-site 134..139
FT /note="N-myristoylated"
FT Modified-site 153..158
FT /note="N-myristoylated"

PN W0200175119-A2.

PD 11-OCT-2001.

XX 02-APR-2001; 2001WO-US10720.

XX 31-MAR-2000; 2000US-193920P.

PA (MILL-) MILLENNIUM PHARM INC.

PI Meyers RA, Rudolph-Owen LA;
XX WPI: 2001-626438/72.
DR N-PSDB; AAT10573.
XX
PT Novel isolated 21509 and 33770 polypeptides belonging to human
PT dehydrogenase family members, useful for treating cancer, diabetes,
PT atherosclerosis, glomerulonephritis, Crohn's disease, cirrhosis,
PT multiple sclerosis -
XX
PS Claim 1(a); Fig 2; 146pp; English.
XX
CC The present sequence is that of a novel human dehydrogenase,
CC designated 21509. The protein has a significant number of
CC structural characteristics in common with members of the
CC dehydrogenase/oxidoreductase family. Its expression pattern
CC suggests a role in tumour development. The invention provides
CC 21509 and 33770 nucleic acids, antisense molecules, recombinant
CC expression vectors, host cells and transgenic animals in which a
CC 21509 or 33770 gene has been introduced or disrupted. It also
CC provides 21509 and 33770 proteins, fusion proteins, antigenic
CC peptides and antibodies, and methods for screening for compounds
CC that modulate the expression or activity of 21509 or 33770
CC polypeptides or nucleic acids. Such modulators are used in methods
CC for inhibiting the proliferation or migration, or inducing the
CC killing, of 21509- or 33770-expressing cells, especially the
CC hyperproliferative and/or metastatic cells of a soft tissue tumour,
CC solid tumour or metastatic lesion, especially ovarian cancer, colon
CC cancer, lung cancer and liver cancer (claimed). Modulator
CC compounds are also used in claimed methods of modulating fatty acid
CC biosynthesis or retinoid biosynthesis in a cell. 21509 and 33770
CC nucleic acids can also be used to prepare diagnostic probes and in
CC gene (including antisense) therapy.
XX
SQ Sequence 237 AA;

Query Match 24.1%; Score 314; DB 22; Length 237;
Best Local Similarity 32.0%; Pred. No. 1.9e-22;
Matches 81; Conservative 41; Mismatches 105; Indels 26; Gaps 5;

```

QY          12  VAVITGASGLATAERLVGGASAVLLDPPNSGGEQAARKIGNCVFAPADTSKDV 71
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB          4  VCAIFGSGKIGIRAAVQALMARQYRLAIARNEEGAKAAADLGSDHIAFSCD 63
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY          72  CFALALAKGKRGFRVAVNACGI-----AVASKYNNLKKGTHTLEDQRVIDNLMGTF 126
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB          64  QNTPEEMEKHGRVNFVNAAGINRFDGLLVKTKT-----EDMVSQLHNLGSM 112
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY          127  NVIRLVAGEMQNEPDQGGQGVIIINTASVAAFEGVQQAAYSASKGIVGMTPIADL 186
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB          113  LTRKAMRAMIQ-----QGGSIVNVSIVGLKNGSGQSYSAKSGIVGFSRLAKEV 166
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY          187  AFIGRVKTIARGLGTPLTSLPKVSNFLASQVFPFSRIGDPAEVAHLVQAIIENPFL 246
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB          167  ARKKIRVNVAPGVYHTDKTKLEE---HLKKNIPL-GREGETIEVAHAYVFLESYI 222
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY          247  NGEVIRLDGAIRM 259
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB          223  TGHVLVVDGLOL 235
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

RESULT 17
AAY54422
ID AAY54422 standard; Protein; 248 AA.

XX AAY54422;

DT 06-APR-2000 (first entry)

XX Amino acid sequence of a beta-ketoacyl-ACP reductase protein.

KM Beta-ketoacyl-ACP reductase; Type II fatty acid synthetase;
KM stereoselectivity; 4-chloroacetate acid ester;

KM (S)-4-halo-3-hydroxybutyric acid ester; 4-halo-acetoacetic acid ester;
KM beta-ketoacyl-acyl carrier fatty acid reductase; acetoacetyl-CoA reductase;
KM polybeta-hydroxy fatty acid biosynthesis; optically active;
KM 4-halo-3-hydroxybutyric acid ester.

OS Bacillus subtilis.

PN EP955375-A2.

PD 10-NOV-1999.

PF 10-MAY-1999; 99EP-0109403.

PR 08-MAY-1998; 98JP-0126507.

PR 21-OCT-1998; 98JP-0300178.

PR 05-APR-1999; 99JP-0098205.

PA (DAICEL CHEM IND LTD.

Yamamoto H;

WPI, 2000-118183/11.

N-PSDB; AA245749.

Producing optically pure (S)-4-halo-3-hydroxybutyric acid ester -

Claim 6; Page 19-20; 34pp; English.

The present sequence represents a beta-ketoacyl-ACP reductase protein of Bacillus subtilis. The beta-ketoacyl-ACP reductase enzyme constitutes a type II fatty acid synthetase. The enzyme has an extremely high reducing activity and stereoselectivity towards 4-chloroacetoacetic acid ester. The specification describes a method for producing a (S)-4-halo-3-hydroxybutyric acid ester. The method comprises CC asymmetrically reducing 4-halo-acetoacetic acid ester or its CC derivative with beta-ketoacyl-acyl carrier protein reductase CC constituting type II fatty acid synthase, or acetoacetyl-CoA CC reductase constituting the polybeta-hydroxy fatty acid biosynthesis CC system. The novel method is used to produce optically active CC 4-halo-3-hydroxybutyric acid ester, with a high purity.

Sequence 248 AA;

Query Match 24.0%; Score 313.5; DB 21; Length 248;

Best Local Similarity 29.7%; Pred. No. 2.3e-22;

Matches 76; Conservative 55; Mismatches 100; Indels 25; Gaps 6;

13 AVITGGSGTGLTAERLVGQASAVLLDPNSGGEAQA-----KTIQNNCFAPADY 65

9 AYTGSARGIGRSLALALAKGANV---VYSGNPAKANEVDEIKSMGRRAIAKADY 65

66 TSEKDVOTALALAKGFRVDVAVNCAGIAVASKTYNLKKQTHLEDFQRLVDVNLMT 125

66 SNEEDVQNMKEITLSTYFSTIDILVNNAGITRDLIMRKE-----DEMDVIVINILKGV 119

126 FNYTRIVAGEMGNPEPOGGRGVITNTASVAFEGOVQAAYASAKSGIVGWTLDIARD 185

120 FNCIKAVTRQMKO-----RSGRIIVSSIVGSGNPGQANVAAKAGVIGLTKSSAKE 173

186 LAPIGIRVMTIAGLEFGTPLLTSLEPKVSNFLASQVFPFSRLGDPAEYAHVQAITE-- 243

174 LASNSITVNAIARGFISTDWTDLAKADQDEMLKQIPL-ARFGSPDSVSSVTFLLASEGA 232

244 PFLNGEIVIRLDGAIKM 259

233 RYMGQTLHIDGKVM 248

XX 29-OCT-2001 (first entry)

XX Putative P. abyssi dehydrogenase #8.

XX Hyperthermophilic archaeon; hyperthermophilic protein.

XX Pyrococcus abyssi.

XX FR2792651-A1.

XX 27-OCT-2000.

PF 21-APR-1999; 99FR-0005034.

PR 21-APR-1999; 99FR-0005034.

PA (CNRS) CNRS CENT NAT RECH SCI.

(IFRE-) IFREMER INST FR RECH EXPL MER.

Porterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O;

Querellou J, Weissenbach J, Saurin W, Heilig R;

WPI, 2001-126236/14.

New nucleotide sequences isolated from Pyrococcus abyssi encode proteins useful in industry -

Claim 7; Pages 1087-1088; 1657pp; French.

The present invention relates to the genomic sequence of Pyrococcus CC abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi is CC a hyperthermophilic archaeon, which is isolated from deep-sea CC hydrothermal vents. The present sequence is one such P. abyssi protein. CC The proteins of the present invention have various potential industrial CC uses, since the proteins are stable at very high temperatures, some up to CC 110 degrees centigrade. CC Note: This patent is in the same patent family as WO200065062, which CC contains additional sequences as shown in AAB99132-AAB99143, CC AAH75903-AAH75920 and AAG66436.

Sequence 241 AA;

Query Match 24.0%; Score 312.5; DB 22; Length 241;

Best Local Similarity 34.1%; Pred. No. 2.8e-22;

Matches 87; Conservative 47; Mismatches 92; Indels 29; Gaps 7;

8 VGLVAVITGGSGTGLTAERLVGQASAVLLDPNSGGEAQA-----VF 60

4 LKGRVALLITGASRGIGRAIAIEIAKRGVNVVINTRSN---BEAKKIEELCRQGVETLL 60

61 APADVTSEKDVOTALALAKGFRVDVAVNCAGIAVASKTYNLKKQTHLEDFQRLVDY 120

61 VKADVSNBEVEYEMVKYIDKFRGIDILINNAGI--LCKT---KDPLEVDDEEDRVISV 115

121 NIMGTFNYTRIVAGEMGNPEPOGGRGVITNTASVAFEGOVQAAYASAKSGIVGWTLD 180

116 NIKGAFITQEVLRM-----KRGRIYNASINAGKDGQVGPHTAAKGGILALTF 166

181 PIARDLAPIGIRVMTIAGLEFGTPLLTSLEPKVSNFLASQVFPFSRLGDPAEYAHVQA 240

167 NIARILAP-NIIYNVAAAGPVDWTLSSMKR-----MKTKSLTGDIAPKPEVAAHVAIFL 221

241 IENPFLNGEIVIRLDG 255

222 LENDHITGEVDVNG 236

RESULT 18

AAB96397 standard; Protein; 241 AA.

AC, AAB96397;

RESULT 19

AAU28156 standard; Protein; 237 AA.

AC, AAU28156;

XX	18-DEC-2001 (first entry)	
DE	Novel human secretory protein. Seq ID No 325.	
XX	Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; fertility; analgesic; pain; antigen.	
OS	Homo sapiens.	
XX	WO200166689-A2.	
PN	13-SEP-2001.	
PD	05-MAR-2001; 2001WO-US04942.	
XX	07-MAR-2000; 2000US-0519705.	
PR	19-MAY-2000; 2000US-0574454.	
PR	17-JUN-2000; 2000US-0596193.	
PR	14-JUL-2000; 2000US-0616847.	
PR	19-SEP-2000; 2000US-0665363.	
PR	20-OCT-2000; 2000US-0693267.	
XX	(HYSE-) HYSEQ INC.	
PA		
XX	Tang YF, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;	
PI	Zhao Qa, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;	
PI	WPI; 2001-589934/66.	
DR	N-PSDB; AAS45056.	
XX	Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders -	
PT		
PT		
XX	Example 4; SEQ ID No 325; 107pp; English.	
PS		
XX	The invention relates to novel isolated human secreted polypeptides (I) and polynucleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses, and is involved in increasing haematopoiesis, stem cell survival, bone growth and remodeling. (I), (II) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, and amyotrophic lateral sclerosis. In addition, (I) is involved in chemotactic or chemokinetic activity, regulation of haematopoiesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease. Furthermore, (I) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. In addition, (I) affects biorhythms or circadian cycles of rhythms, fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid protein, carbohydrate, vitamins, minerals, provides	
CC	analgesic effects or other pain reducing effects, immunoglobulin like	
CC	activity and can act as an antigen in a vaccine composition to raise an	
CC	immune response. AAU28020-AAU28395 represent novel human secreted protein	
CC	amino acid sequences of the invention.	
XX		
SQ	Sequence 237 AA:	
QY	Query Match 23.9%; Score 312; DB 22; Length 237;	
Db	Best Local Similarity 31.6%; Pred. No. 3e-22;	
QY	Matches 80; Conservative 42; Mismatches 105; Indels 26; Gaps 5;	
Db	4 VCAVFGSGRIGRAVAVQALMARRGYRLAVIARNLKGAAGDGLGDFHAFSCDVAKKHV 63	
QY	12 VAVITGASGLGATNERLVGGASAVLIDLPNSGGEAOKLGNVCYFAPADVYSEKV 71	
Db	72 QFALALAKGKRGVDAVAVNCAGI-----AVASKTYNLKKGTHTLEDFOFVLDVIMLGT 126	
QY	64 QNTFEMKEHLGRVNLVNAAGINRGGLVTKT-----EDMSQHLNLSGM 112	
Db	127 NVIRLVAGENGQNEPDGQGVYINTASVAEFEGVGQAAYSASRKGIVGKTLPIARDL 186	
QY	113 IFCRKAMRMVIOQ-----QGSGIVNVGSIIVGKNGSGOSVYSASRKGIVGFSRALAKEV 166	
Db	187 APGIRVMTIAPGLFCTPLTSLPEKVSNFLASQVFPRLDPAPVYAHLYQATINPLT 246	
QY	167 ARKKIRVNVVAPGFVITDMTKLKEE---HLKKNIFL-GRFGETIVAAVYFLESEPTI 222	
QY	247 NGEVIRLDGAIRM 259	
Db	223 TGHVLYVDGGL 235	
RESULT 20		
AA19928		
ID	AA19928 standard; Protein; 237 AA.	
XX	AA19928;	
XX		
DT	19-MAR-2001 (first entry)	
XX	Human oxidoreductase OXR-3.	
XX		
KW	OXRD-3; human; oxidoreductase; dehydrogenase; cell proliferation;	
KW	neurological disease; smooth muscle disease; autoimmune disease;	
KW	inflammation; antiproliferative; neuroprotective;	
XX	immunosuppressive; antiinflammatory; therapy; diagnosis.	
OS	Homo sapiens.	
PH	Key Location/Qualifiers	
FT	Misc-difference 66	
FT	/note= "O-phosphorylated"	
FT	Misc-difference 95	
FT	/note= "O-phosphorylated"	
FT	Misc-difference 114	
FT	/note= "O-phosphorylated"	
FT	Region 3..184	
FT	/note= "short-chain dehydrogenase signature"	
PN	WO200071679-A2.	
XX		
PD	30-NOV-2000.	
XX		
PF	19-MAY-2000; 2000WO-US13879.	
XX		
PR	20-MAY-1999; 99US-0135049.	
PR	27-MAY-1999; 99US-0136740.	
XX	(INCY-) INCYTE GENOMICS INC.	
PA		
PI	Yue H, Tang YT, Baughn MR, Lu DM;	
XX	WPI; 2001-025146/03	

DR N-PSDB: AAA89187.
 XX
 PT New human oxidoreductase proteins useful for diagnosing, treating or
 PT preventing proliferative, neurological, genetic, smooth muscle,
 PT autoimmune or inflammatory disorders associated with abnormal
 PT expression of oxidoreductase proteins
 XX
 PS Claim 1(a); Page 83; 95pp; English.
 CC The present sequence is that of human oxidoreductase OXR-3, as
 CC deduced from a cDNA clone (see AAA89187) isolated from a lung tumour
 CC cDNA library. The protein shows homology to Escherichia coli
 CC 3-oxoacyl-(acyl)-carrier protein, and includes a short-chain
 CC dehydrogenase signature. OXR-3 is expressed in nervous, reproductive,
 CC cardiovascular and gastrointestinal tissue, and may be involved in
 CC cell proliferation and inflammation. The invention provides OXR-1
 CC to -8 polypeptides (see AAA19926-33) and polynucleotides (see
 CC AAA89185-92). It also provides methods for using these polypeptides
 CC and polynucleotides for diagnosing, treating or preventing disorders
 CC associated with expression of OXR, especially cell proliferative,
 CC neurological, genetic, smooth muscle, and autoimmune/inflammatory
 CC disorders. The proteins can also be used to screen for agonists
 CC and antagonists useful for treating these conditions, while
 CC antibodies that bind to OXR may be used for diagnosis or in assays
 CC to monitor patient treatment.
 XX
 SQ Sequence 237 AA;
 Query Match 23.9%; Score 312; DB 22; Length 237;
 Best Local Similarity 31.6%; Pred. No. 3e-22;
 Matches 80; Conservative 42; Mismatches 105; Indels 26; Gaps 5;
 QY 12 VAVTGGASGIGLATARLYGQASAVLLDLPNSGGRAQAKKGNVCYRPAVYSEKY 71
 Db 4 VCAVFGGSRGIGRAVVAQIMARKGYRLAVIRNEGAAAGDLAGSHLAFSCVAEHDV 63
 QY 72 QATALAKGKFGRDVAVNCAGI-----AVASKTYNKKQGTHTLEDFQVLDVNLGTE 126
 Db 64 QNTEEMKHLGRNPLVNAAGINRDLVIRTK-----EDMSQLHTNLLGSM 112
 QY 127 NVIRLVAGMGQNEPDGQGRGVYIINTASVAAPFGQQAAYSASKSGITGMPLIARDL 186
 Db 113 LTRCAARKTMIOQ-----QGGSIVNGSIVGLKNSGQSVYSASKGLVGFSPALAKEV 166
 QY 187 APGIRVMTIAPGLFETPLTSLPEKYSNFLASQVPPSRGLDPAEYFAHLVQAIIENPFL 246
 Db 167 ARKKIRVAVAPFGVHDMTKDEE---HLKKNIPF-GRGERTIEVAHNAVFLLESPYI 222
 QY 247 NGEVIRLDGAIRM 259
 Db 223 TGHVLYVDGLQL 235
 Db
 RESULT 21
 ID ABB48892 standard; Protein: 247 AA.
 AC ABB48892;
 XX 05-FEB-2002 (first entry)
 XX Listeria monocytogenes protein #1596.
 DE Listeria monocytogenes protein #1596.
 XX Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
 KW vitamin B12; bacterial infection; disease.
 XX Listeria monocytogenes.
 OS
 XX WO200177335-A2.
 XX
 XX 18-OCT-2001.
 PD
 XX 11-APR-2001; 2001WO-FR01118.
 PF

XX
 PR 11-APR-2000; 2000FR-0004629.
 XX
 PA (INSP) INST PASTEUR.
 XX
 PI Buchrieser C, Frangeul L, Couve E, Rusnok C, Feishi H, Dehoux P;
 PI Duseigneur O, Chetouani F, Nedjati H, Glaser P, Kunst F, Cossart P;
 PI Daniels J, Goebel W, Kieft J, Kuhn M, Ng E, Vazquez-Boland JA,
 PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
 PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
 PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
 PI Madueno E, De Pablos B, Wehlund U, Kaerst U, Entian K, Hauf J;
 PI Rose M, Voss H;
 DR WPI; 2002-010914/01.
 XX
 XX Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
 XX and prevention of Listeria and related bacterial infections, and
 XX related polypeptides
 PS Claim 6; SEQ ID No 1597; 192pp; French.
 XX
 XX The present invention relates to the genome sequence of Listeria
 XX monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
 XX it are useful for selecting probes and primers for detecting genes in L.
 XX monocytogenes and related organisms, and for studying genetic
 XX polymorphisms and other genomes. The present sequence is a protein
 XX encoded by the genome sequence of the present invention. Proteins
 XX expressed from the genome sequence are useful for raising specific
 XX antibodies. Identification of L. monocytogenes and related organisms, and
 XX for biosynthesis and biodegradation, especially biosynthesis of Vitamin
 XX B12. The genome sequence and proteins encoded by it are also useful for
 XX selecting compounds that regulate gene expression and cell replication
 XX and modulate L. monocytogenes-related diseases. In addition, the genome
 XX sequence and proteins encoded by it are useful in pharmaceutical and
 XX vaccine compositions for the treatment or prevention of infections by L.
 XX monocytogenes and related organisms.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 247 AA;
 Query Match 23.5%; Score 306.5; DB 23; Length 247;
 Best Local Similarity 32.0%; Pred. No. 1.1e-21;
 Matches 85; Conservative 45; Mismatches 103; Indels 33; Gaps 7;
 QY 7 SVKGLVAVITGGASGIGLATARLYGQASAVLLDLPNSGGRAQAKKGNVCYRPAVYSEKY 58
 Db 2 TLQGRVAVYVITGGSRGIGRIALINLAEGANIFE-----NYNGSPEAAEYAKILVAHGEV 57
 QY 59 VRAPADYTSKDYQTLALAKGKFGRDVAVNCAGIYASVASKTYNKKQGTHTLEDFQVLD 118
 Db 58 EAMKAVYALAEVDPAFFKQAIERFGRVDTLVNNAGITRDNLMARKKE-----DWDVYI 111
 QY 119 DVNLMGTFVYIRLVAGMGQNEPDGQGRGVYIINTASVAAPFGQQAAYSASKSGITGM 178
 Db 112 NINLKGTFCTKAVSTMMKQ-----RAGKIINNASVYGLIGNAGQANVYASKAGVIGL 165
 QY 179 TLPIARDLAPIGIRVMTIAPGLFETPLTSLPEKYSNFLASQVPPSRGLDPAEYFAHLVQ 238
 Db 166 TKTTARELAPRGIVNAVAPGFTTMDTKLDEKTEKMAIOIP-----LSANGTTEIDIAN 221
 QY 239 AIT-----ENPFLNGEYIRLDGAIRM 259
 Db 222 AVLFLASDASKYITGQTLISVDGGMV 247
 Db
 RESULT 22
 ID AAY95746 standard; Protein: 247 AA.
 AC AAY95746;
 XX
 XX AAY95746
 AC AAY95746;

XX 25-OCT-2000 (first entry)
 DT
 XX Bacillus megaterium 3-keto-acyl-CoA reductase Phab.
 DE
 XX Polyhydroxyalkanoate; polyhydroxybutyrate; transgenic plant; Phab;
 KW 3-keto-acyl-CoA reductase.
 XX
 OS Bacillus megaterium.
 OS
 PN WO200040730-A1.
 XX
 PD 13-JUL-2000.
 XX
 PF 07-JAN-2000; 2000WO-US00364.
 XX
 PR 07-JAN-1999; 99US-0115592.
 XX
 PA (UYMA-) UNIV MASSACHUSETTS.
 XX
 PI Cannon MC, Cannon FC, Mccool GJ, Valentin HE, Gruys KJ;
 XX
 DR WPI: 2000-532624/48.
 DR N-PSDB: AAA50142.
 XX
 PT New nucleic acid fragment encoding proteins involved in
 PT polyhydroxyalkanoate (PHA) biosynthesis, useful in the production of
 PT transgenic plants or recombinant plant cells which can express PHAs
 PT such as polyhydroxybutyrate -
 PS
 PS Claim 85; Page 137-138; 153pp; English.
 XX
 CC The present sequence is that of Phab, a 3-keto-acyl-CoA-reductase
 CC protein of Bacillus megaterium. The sequence was deduced from an
 CC open reading frame identified in an isolated 7,916 bp fragment of
 CC B. megaterium strain 11561 genomic DNA (see AAA50142). The 7,916 bp
 CC DNA fragment includes genes encoding proteins (see AA95743-47)
 CC involved in polyhydroxyalkanoate (PHA) biosynthesis. Nucleic acids
 CC encoding these proteins are useful for creating transgenic plants or
 CC recombinant host cells which have the capability of expressing PHAs
 CC such as polyhydroxybutyrate, polyhydroxyvalerate,
 CC polyhydroxyhexanoate, polyhydroxyoctanoate, polyhydroxydecanoate or
 CC their copolymers. Claimed methods for preparing a PHA involve
 CC obtaining a plant or a cell comprising a nucleic acid sequence
 CC a 3-keto-acyl-CoA reductase (especially the present sequence), and
 CC a nucleic acid encoding a PHA synthase (see AA95747), and growing
 CC the plant or cell under conditions suitable for PHA production.
 CC
 XX
 SQ Sequence 247 AA:
 Query Match 23.2%; Score 303; DB 21; Length 247;
 Best Local Similarity 29.1%; Pred. No. 2.4e-21;
 Matches 78; Conservative 59; Mismatches 93; Indels 38; Gaps 9;
 QY 7 SVKGIATVITGGASGIGLTAETRIYVQG-----ASAVLLDPNNGGEGQAK 53
 DB 3 TLGGKVAIVTGGSKGGAALITRELASNGYKAVANNSSKESDAIYKEIKDNGER---- 58
 QY 54 LGNNCYFAPADVTSEKDVOTALALAKGFRVDVAVNAGIAVASKTYNLRK-GQTHLE 112
 DB 59 -----IAVQADVSYYQAKHLEETRAFGOLDIIVNNAIGI---TRDSFRKIGE-----E 106
 QY 113 DFRQVLDVNLMTGFNIRLVAGMGNEEDDGGQKRVITNTKSVAFSEQVGOAAVSAK 172
 DB 107 DMKKVIDVNLHSHVYNTSALTLHLESE---GGR---VINISITIQAGGFGQNTSAK 160
 QY 173 GGIVGMTLPJARDLIGIRVMTIAPLGTPLTSLPKRVSNFLASQVFPFSRLGDPAE 232
 DB 161 AGHLGTTKSLALELATAGTVNNAICGFIETEMVMAIPEDVRAKIYAKIP-TRRLGHAE 219
 QY 233 YAH-LVQATLENFPLNGEVIYRLDGAIRM 259
 DB 220 IARGVYLLAKDGAVIITGOOLNINGLYM 247

RESULT 23
 AAU28296
 ID AAU28296 standard; Protein: 288 AA.
 XX
 AC AAU28296;
 XX
 DT 18-DEC-2001 (first entry)
 DE
 DE Novel human secretory protein, Seq ID No 653.
 XX
 KW Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
 KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;
 KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 KW fertility; analgesic; pain; antigen.
 XX
 OS Homo sapiens.
 OS
 OS WO200166689-A2.
 PN
 PN 13-SEP-2001.
 XX
 PD 05-MAR-2001; 2001WO-US04942.
 XX
 PF 07-MAR-2000; 2000US-0519705.
 PR 19-MAY-2000; 2000US-0574454.
 PR 17-JUN-2000; 2000US-0596193.
 PR 14-JUL-2000; 2000US-0616847.
 PR 19-SEP-2000; 2000US-0665363.
 PR 20-OCT-2000; 2000US-0693267.
 XX
 PA (HYSE-) HXSEQ INC.
 XX
 PI Tang YF, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
 PI Zhao QH, Yang Y, Drmanac RT, Zhang J, Chen R, Xie AJ, Wang J;
 XX
 DR WPI: 2001-589934/66.
 DR N-PSDB: AAS45196.
 XX
 PT Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders -
 PT
 XX
 PS Example 2; SEQ ID No 653; 107pp; English.
 PS
 CC The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing haematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I) (II) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions,
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and

CC disorders, including severe combined immunodeficiency (SCID), bacterial or
CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
CC reactions and conditions such as asthma or other respiratory problems.
CC In addition, (7) affects biorhythms or circadian cycles of rhythms,
CC fertility, metabolism, catabolism, anabolism, storage or elimination of
CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
CC analgesic effects or other pain reducing effects, immunoglobulin like
CC activity and can act as an antigen in a vaccine composition to raise an
CC immune response. AAU26020-AAU28395 represent novel human secreted protein
CC amino acid sequences of the invention.

SQ Sequence 288 AA;

Query Match	23.0%;	Score 300.5;	DB 22;	Length 288;
Best Local Similarity	29.9%;	Pred. No. 5.3e-21;		
Matches	84;	Conservative	44;	Mismatches 110;
				Indels 43;
				Gaps 6

OY 1 MAACRSVKGLVAVTITGGASGIGLATAERLVGGASAVLLDLPNSGGGAQAKKLTGNCF 60
||| ||| :||| :||| :||| :||| :
Db 10 MATGR-YAGCAVAVTGGGRRGAGIVRAFAVNSGARVITCDKDESGRALFQETPGCLL 68

QY 61 APADVTSEKDVQITALALAKGKFGRDVAVVNCAGIAVASKTYNLKCGOTHTLEDFOBYLDV 1200
 : ||| | ||| : : ||| : || |
 Db 69 SFCVYTOEDDVKTIVSETTRBFGRI.DCVVNVNNGHHBDB-----OPDETSAGCEPOLLET 1233
 : ||| | ||| : : ||| : || |

121 NIMGTFNTRLVAGENGQNEPDGGQGRVITINTASVAAFEGQVGQAAYSASKGCIYGMTL 180

22 181 PIARDLAPIGIRVMTIAPGIEGTPILTSLEPKVSNEIASQYFP----- 224

DP 1 // ALALDESPGVAVRANCISPGNIWTPMEE-----LAALMPDPRAIIRREGHLAQGRSGV 228
 QY 225 -----SRLGDPAEY-AHLVQAIENPFNGEVIRLDGAIRM 259

Db 229 QIDPLGRMGQPAEYGAAYFLASEANFCTGIXLVTGGAEL 269

AB039667
ID AB039667 standard; Protein; 263 AA.
XX

AC	ABP39667;
XX	
DT	24-JUL-2002 (first entry)

DE	XX	KW
Staphylococcus epidermidis ORF amino acid sequence, SEQ ID NO:4512.		
Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;		

KW	antibacterial; gene therapy.
XX	
OS	Staphylococcus epidermidis.
VV	

PN	US6380370-B1.
XX	
PD	30-APR-2002.

AA	
PF	13-AUG-1998; 98US-0134001.
XX	
PR	14-AUG-1997. 97US-055779D

PR 08-NOV-1997; 97US-064964P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.

aa Doucette-Stamm LA, Bush D;
PI
XX
DR WPI: 2002-381255/41.

DR N-PSDB; ABN92212.
XX
PT Novel isolated nucleic acid encoding a Staphylococcus epidermidis

XX

PS Disclosure; SEQ ID 4512; 267pp; English

ABR950533 to ABR953374 represent *Staphylococcus epidermidis* open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABR95114 to ABR95960. The *S. epidermidis* sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly *S. epidermidis* infections. The sequences can be used to screen for compounds able to interfere with the *S. epidermidis* life cycle or inhibit *S. epidermidis* infection. Not form part of the claimed invention.

CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC USPTO web site.

Sequence 263 AA

Query Match	22.6%	Score 295;	DB 23;	Length 265;
Best Local Similarity	32.3%	Pred. No. 1.6e-20;		
Matches	86;	Conservative 42;	Mismatches 104;	Indels 34;
			Gaps	6;

```

Qy 12 VAVITGASGICLATAPERTLVGQASAVLIDLPNSGGEAQAKL---GNCCYFAPADYTS 688
    |||:| | :|| | | | | : | :| | | | | | | | | | | | | | | | | | | |
Db 11 VAVVTGAAGGICGLKIAPERTLVFDGYSIALVDNFENEYAKESAEKLSKGGQEAFAFKADY 700

```

Qy 69 KDVOTALALAKGEGRYDAVAVNAGIAVASKTYNLKKQTHTLDEFQRVLVDYMLMGTFNV 12
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 71 DOVESSTNOVEHEGGDINLVNNAGIGPMTP-----FESTPEENOVVGCGVNGSGEFG 12

129 IRLVAGEMGNEPDDGGORGVITINTASVAAFEQVGQAAYSAKSGIVGWTLP IARDLP 18

189 IGIRVMTIAPGLFGTPLLTSLPEKVSNFLASQVFP-----SRLGDPAEYA 2

DB 180 KNITVAFAFGIVETPMKGIAR ----LAEENQPMENGMKQFNDQIALRLSKPBEVA 2
QY 235 HLVAAT--ENPFLNGEYIRLDGAIR 258

Db 236 NVSEFLAGSDSDYITGQPIIVDGMR 261

RESULT 25
AAR89323
ID AAR89323 standard; Protein: 315 AA.
XX

AC	AAR89323;
XX	
DT	13-APR-1996 (first entry)

RA Rape leaf beta-ketoacyl-ACP-ketoreductase.
 DE Rape leaf beta-ketoacyl-ACP-ketoreductase.
 XX Rape leaf beta-ketoacyl-ACP-ketoreductase: beta-ketoreductase:
 KW Rape leaf beta-ketoacyl-ACP-ketoreductase: beta-ketoreductase:

KW plasmid purl6.2; cdna library; *Escherichia coli*; vector;
KW plastid; stroma; transit peptide; cassette; antisense; oilseed;
KW transgenic plant; crop improvement; lipid; metabolic engineering;

XX
XX
OS *Brassica napus.*
XX

Key	Location/Qualifiers
FT Peptide	1..55
FT	/note= "Transit peptide"
XY	

PN	W09602652-A2.
XX	
PD	01-FEB-1996.

AA 17-JUL-1995; 95WO-GB01678.
PF
XX
PR 20-JUL-1994: 94GB-0014622.

XX
PA (ZENE) ZENECA LTD.
XX

PI Chase D, Elborough K, Fentem PA, Slabas AR, White A;
 XX WPI; 1996-105914/11.
 DR N-PSDB; AAQ99305.
 XX

PT New isolated rape beta-ketoreductase DNA - used to develop plants
 XX with lower or higher oil contents or with altered oil compsn.
 XX

PS Claim 2; Page 16; 29pp; English.

CC The sequence corresponds to a rape leaf beta-ketoreductase encoded
 CC by a cDNA insert in plasmid pJRL6.2 in Escherichia coli XL1-Blue.
 CC A plastid stroma targeting transit peptide is present. DNA
 CC encoding the protein may be inserted in a vector or expression
 CC cassette in sense or antisense orientation for expression in an
 CC oilseed plant, e.g. for production of transgenic rape plants with
 CC low or modified oil content, diversion or metabolism to alternative
 CC storage compounds, e.g. starch, protein or engineered polymers, or
 CC production of plants with enhanced oil content. The DNA may also
 CC be used as a probe to obtain similar genes from other plants. The
 CC transit peptide may be used to direct other proteins to leaf
 CC plastids.
 CC

SQ Sequence 315 AA;

Query Match 22.6%; Score 295; DB 17; Length 315;
 Best Local Similarity 30.5%; Pred. No. 2e-20;

Matches 80; Conservative 44; Mismatches 116; Indels 22; Gaps 6;

OY 4 ACRSVKGLVAVITGGAGSLGATRAERLYVGASAVLLDLPNSGGEA-----QAKKIGNNC 58
 DB 66 AVPRVESPVVVVVGASRGKIGKALRLSL-GRAGCKVLVNVARSASKEAEVSKQTEAYGGQA 124
 OY 59 VFAPADVTSEKDYOTALAKKGFGRVAVANCAGIATAVASKTYNLKKGQTHLEDFQRYL 118
 DB 125 ITFGGVSKEDVEMAMKKTALDAMGTIDVVVNNAGITRDLLIRMKKSQ-----WDEVI 178
 OY 119 DVNLMTFFNVIRLVAGEMGONRPPDGGQGVIIINTASVAFEGGVGOAAYSASKGIYGM 178
 DB 179 DLNLTGVFLCTQAATKIMRK-----RKGRINIISVGLIGNIGQANYAARAGYIGF 232
 OY 179 TLPIARDLAPIGIRMTIAPGLFTPLTSLPEKVSNFLASOVFPFRLGDPAYAYALVQ 238
 DB 233 SKTAREGASRNINNVVCPFIASDMTAKLGEDEMEKKIIGTIFL-GRYGPEDVAGIVE 291
 OY 239 AILENP---FLNGEVIRLDGAI 257
 DB 292 FLALSPASVITGQAFITDGI 313

Search completed: June 23, 2003, 14:28:35
 Job time : 41.6667 secs

RESULT 10
F83098
Probable short-chain dehydrogenase PA4389 [imported] - Pseudomonas aeruginosa (strain PA
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: F83098
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Micoicuchi, S.D.; Warrenner, P.; Hickey, M.T.; B
adman, S.; Yun, Y.; Brody, L.L.; Coulter, S.N.; Folgar, K.R.; Kas, A.; Larbig, K.; Lim,
Loy, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: AB2950; MUID:2043737; PMID:10984043
A:Accession: F83098
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-252 <SRO>
A:Cross-references: GB:AB004854; GB:AB004091; NID:99950606; PIDN:AG07777.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA4389
C:Superfamily: r1b1tol dehydrogenase; short-chain alcohol dehydrogenase homology

```

Query Match          27.2%:  Score 355:  DB 2:  Length 252:
Best Local Similarity 35.1%:  Pred.No. 2,9e-20:
Matches 94:  Conservative 40:  Mismatches 100:  Indels 34:  Gaps 7:

      Oy      8 VKGLVAITGTGASGLGATARTLRVGGGASATLIDLPN-----SGGEAQAARKLG 55
      Db      3 LKDVYIITIGSCGGLGRAMGEYLAGKGRRLATLVLDLNTRELRDEAFAACAGAGDRA--- 58
      Oy      56 NNCFAPADVNSEKDYGTALALAKGKGRVDAVNAAGIAVASKTYMLKKQGFH--TLFD 113
      Db      59 -----LYCNVADEQVTHMAQVASDFGAINGLVNNAGILRLDGLITIKYKQDQLSKMLAQ 113
      Oy      114 FQRYLDVNLMTGTEFNIVIRLVAGEGQ--NEPDQGGQRYIINTASVAAFEGGVGAAYSAS 171
      Db      114 MQSYIDVNLTVGFCTREVAAKMETLKN-----GAIVNIISSIR-AGNMGAQNSAA 165
      Oy      172 KGGIVGMLPLPIARDLAPGIRKMTIAPGLEFPTPLTTSPEEVANFLASQVFFPRLGDPA 231
      Db      166 KAGVAADIVWAKELARYGIRKAVAPQFIETETWAGMKPRLAKMTAGIPL-KRMGKV 224
      Oy      232 EXAHLVQAIIENPFLNGEVIIRLDGAIRM 259
      Db      225 EIAHSVAIIFENDIYTGRLVELDGL 252

RESULT 11
F97338
3-keacetyl-acyl carrier protein reductase [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C:Accession: F97338
R:Rolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daily, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
U: Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo-
A:Reference number: B96900; MUID:21359325; PMID:21359325
A:Accession: F97338
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <KUP>
A:Cross-references: GB:AE001437; PIDN:AAK81497.1; PTD:q15026670; GSPDB:GN00166
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC3574
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

```

Qy	8	KKGIVANTTGGASGLGATAEHLVGGASAVLLDLPSPGGEAO-----AKKLSNNCFAP	62
Db	5	LSGIVAAVATGGGRCGLGRIALIKLAESANLV-VNRYSESEFOTKLMEIHELGSRAVAVK	63
Qy	63	ADVTSEKDVOITALAKGKRGVDVAVNCGAIVASVTVYLLKKGQHTLEDPOFVLVDNL	122
Db	64	ADISKYDEAEETIIKKALDEYGTVDIILNNAGITKDNILLMKK-----EDPDSIVAVNL	117
Qy	123	MGTNNVRLVAGEGQNEHPPDOGGRGVYIINTASAAPEEGVGGAASAGSKSGIVGMFLPI	182
Db	118	KGAENNCIKHETSRVWLK-----KSGKININISVIGLGNAGOVNYAAAKAGITGMKSV	171
Qy	183	ARDLAPIGIRVMTIAPGLFGTHPLTSLPERVANFLASGVFFPSRLGDAPEAYAHVQAIIIE	242
Db	172	AKELASRGITFVNAVAPGLIKSDMTDALTDKORESIYAAPVL-NKVGAEAEVANLVFLAS	230
Qy	243	--NPLNGEVYRLDGAIRM	259
Db	231	DLSYYITGGVINVVDGAVM	249

RESULT 12
H72219
3-oxoacyl-(acyl carrier protein) reductase - Thermotoga maritima (strain MSB)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence revision 11-Jun-1999 #text change 21-Jul-2000
C:Accession: H72219
C:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hult
Garratt, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
C.M.
Nature 399, 332-339, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: H72219
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-246 <ARN>
A:Cross-references: GB:AE001811, GB:AE000512; NID:g4982291; PIDN:AAJ36790.1; PID:g4982291
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1724
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
E:6-185/Domain: short-chain alcohol dehydrogenase homology <SAB>

Query Match	25.3%	Score 343	DB 2	Length 246
Best Local Similarity	33.7%	Pred. No. 2.4e-19		
Matches	86	Conservative 47	Mismatches 104	Indels 18
			Gaps 5	
QY	8	VKGLVAIVTGGASGIGLATAERLVGQASAVLLDLPNSGGA--QAQKLGNNCFAPAD	64	
DB	3	LEGRKCLITLALGASIGKATTTLLFAQEGATVIAGDISKENTSLVKEAGELGKRDVPYLN	62	
QY	65	VTSEMDQGTALALANGKFRGVDVAVNCAGIAVASKTYLKKRGQHTTEDEPQRLVDNLNG	124	
DB	63	VTDRQGLEEVYKVKYQKTRIDVLVYNNAGITRDALLVYMK-----EDMDAIVINLKG	116	
QY	125	TFNVIRLVAAGENGQNEPDGGQRGVYINTASVAAEFGVQQAAYSASKSGVIGMTLPYAR	184	
DB	117	VENVYQMVVVPYMIK-----RNGSIVNVSSVGVYGPMDQGVNTVAASKAGVGMKTKWAK	170	
QY	185	DLAPIGIRVMTAPGLFCGTPILTSLPEKVANVLASQVPPSRIGDPAEYAHLV--QAITE	242	
DB	171	ELAGNINRINNAVAPFETIETPMTEKIRPEKARETALSRIPL-GFGKPEEVAQVILFLASDE	229	
QY	243	NFLNGEVIARLDGAI	257	
DB	230	SSYVTVGVYIGIDGGL	244	

RESULT 13
C83961

```

C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 03-Aug-2001
C:Accession: C83961
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: AB3650; MUID:20512582; PMID:11058132
A:Accession: C83961
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-246 <STO>
A:Cross-references: GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BA06210.1; GSPDB:GNOC
A:Experimental source: strain C-125
C:Genetics:
A:Gene: fabg
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match      25.7%; Score 335.5; DB 2; Length 246;
Best Local Similarity 34.2%; Pred. No. 9,2e-19;
Matches 90; Conservative 42; Mismatches 102; Indels 29; Gaps 7;

QY 8 VAGLAVITVGASGGLTAERLVGASAVLDPNNGGE-----AQAKLGNVCV 59
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 LOGKRIIVGASRGIGRAIMELAHGANVY---NAGNKEKAKVVAELKEIGVRAI 57

QY 60 PAPADVTSEKDVOTALAKKFGFGRVDVAVNCAGIAVASKTYNKKGOTHTLEDFQRYLD 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 58 AICADVADSESYQAWKERTIDTFGAVDILVNNAGITRDLNLFEMKE-----EDMDAVID 111

QY 120 VINMGTFNIRLVAGEMGONEPDGQGOR-GVITINVAFAFGGVGOAAYASAKSGIYGM 178
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 112 TMLKGVFHCASKAVTRPMK-----QRFGRITINSSVGAIGNAGQANVAAKAGVIGL 164

QY 179 TLPIARDLAPIGIRVWTIAPGLFGPLTSLPEKVANFLASQVPPPSRLGDAEYAHVQ 238
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 165 KTLIAELANRMTIVAVAPGFETIDMGELPEDVKAQMLGIPL-ARLGPPEVAKAVR 223

QY 239 AILEN--PFLNGEVRILDAIRM 259
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 224 FLASDASILTGTITVHNGMVA 246

RESULT 14
TS1084
3-oxoacyl-[acyl-carrier-protein]-reductase (oar-1) [imported] - Neurospora crassa
N:Alternate names: protein B2A19.180
C:Species: Neurospora crassa
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 24-May-2001
C:Accession: TS1084
R:Schulte, U.; Aign, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence database, July 2000
A:Reference number: 225286
A:Accession: TS1084
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-297 <SCH>
A:Cross-references: EMBL:AL390092; GSPDB:GN00116; NCSP:B2A19.180
A:Experimental source: BAC clone B2A19; strain OR74A
C:Genetics:
A:Gene: NCSP:B2A19.180
A:Map position: 6
A:Titrons: 218/1; 249/1
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match      25.7%; Score 335.5; DB 2; Length 297;
Best Local Similarity 31.7%; Pred. No. 1,2e-18;
Matches 97; Conservative 39; Mismatches 103; Indels 67; Gaps 8;

QY 6 RSVKGLVAVTTGASGGLTAERLVGASAVLDPNNGGE-----GGEAG 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 RSLHKOALTTGGSGGLTAERLVGASAVLDPNNGGE-----GGEAG 50

QY 51 AKKLGNCVAPADVTSEKDVOTAL-ALAKGFGFGRVDVAVNCAGIAVAS---RTYNLKGK 106

```

RESULT 16

3-oxoacyl-[acyl-carrier protein] reductase [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp.
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: AB2042
R:Kakeko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi, N.; Shimizu, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
D:Res. 8, 205-213, 2001
A:Title: Complete genomic sequence of the filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AB2042
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-251 <KUR>
A:Cross-references: GB:BA000019; PIDN:BAH73593.1; PID:G17130984; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: fabG
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.7%; Score 334.5; DB 2; Length 251;
Best Local Similarity 33.1%; Pred. No. 1,1e-18;
Matches 91; Conservative 46; Mismatches 97; Indels 41; Gaps 7;

QY 1 MAACGSVGVAVITGASGLGATAEELVGGASAVLIDPNSGG 47
DB 1 MALLSNTLNGVAVITGASRGIGRALELANTYVAVYASSSTADAEVAVETGAGG 60
QY 48 EAQAKKLNVCVAPADVTSEKDVOTATALAKGFRVDVAVNCAGIYASKTYNKKQ 107
DB 61 EAVALK-----ADVQVQVQVNLINGAIDKFRIDILVNNAGITRDLILMKP-- 109
QY 108 THTLEDFORVLDVNLGTFNVRILVAGENGEPGOGGQGVITNTASVAAFEQGVQAA 167
DB 110 ----EDMQAVIDNLNLGFLCTRAVSKMLKQ-----RSGRIITITSVAGCMGPGQAN 159
QY 168 YSASKGCIIVMTLPARDLAPIGIRVMTAPGLFPTPLTSLPEKVANFLASQVPPSR 227
DB 160 YSAAKGVIGFTKVAKKELASRGITVYNAVAPGFIATDMTSLNK---SEGIIQYIPL-GRY 215
QY 228 GDPAEVAHLVQALIEP---FLNGEYIRLDGAI 259
DB 216 GQPEELAGMVRFLADPAAPAYITGOVFNVDGGMV 250

RESULT 17

3-oxoacyl-[acyl-carrier protein] reductase BH3896 [imported] - Bacillus halodurans (strain H84136)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: H84136
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira, N.
D:Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and its reference number: AB3650; MUID:20512582; PMID:11058132
A:Accession: H84136
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-246 <STO>
A:Cross-references: GB:AP001520; GB:BA000004; NID:G10176401; PIDN:BAH07615.1; GSPDB:GN00
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH3896
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.5%; Score 332; DB 2; Length 246;
Best Local Similarity 34.2%; Pred. No. 1.7e-18;
Matches 91; Conservative 40; Mismatches 95; Indels 40; Gaps 8;

QY 8 VKGLVAVITGASGLGATAEELVGGASAVLIDPNSGG 55
DB 3 LNKVAVITGASGLGATAEELVGGASAVLIDPNSGG 58
QY 56 NNCVFPADVTSEKDVOTATALAKGFRVDVAVNCAGIYASKTYNKKQ 115
DB 59 ----SWEDTQKDVKNYINQYIERFELDVYVNNAGITADQNTMTDAQ-----WD 107
QY 116 RVLDVNLGTFNVRILVAGENGEPGOGGQGVITNTASVAAFEQGVQAAVSKGSI 175
DB 108 DVIDVNLKGVFTYQGVITTKRQ-----KRGVILNASSVSGYSGNFGQNTAASKMGV 161
QY 176 VGMTLPARDLAPIGIRVMTAPGLFPTPLTSLPEKVANFLASQVPPSRIGDPAE--- 232
DB 162 NGMTKTAKELGRIYVAVAPGFIPTETKRPKVKVMEKAVL-NRLGTVEVAN 220
QY 233 -VAHLVQALIEPFLNGEYIRLDGAI 257
DB 221 GFAFL-ASDEASTFETITAIIDGV 244

RESULT 18

3-oxoacyl-[acyl-carrier protein] reductase VC2021 [imported] - Vibrio cholerae (strain F82128)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: F82128
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.; Heidelberg, J.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
D:Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: AB2035; MUID:2040683; PMID:10952301
A:Accession: F82128
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-248 <HEI>
A:Cross-references: GB:AE004276; GB:AE003852; NID:9656555; PIDN:AAF95169.1; GSPDB:GN
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2021
A:Map position: 1
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.3%; Score 330.5; DB 2; Length 248;
Best Local Similarity 32.0%; Pred. No. 2.3e-18;
Matches 82; Conservative 54; Mismatches 103; Indels 17; Gaps 5;

QY 7 SVKGLVAVITGASGLGATAEELVGGASAVLIDPNSGG 66
DB 6 NLEKVALVTVGASRGIGRALELANTYVAVYASSSTADAEVAVETGAGG 65
QY 67 SEKVQVOTATALAKGFRVDVAVNCAGIYASKTYNKKQ 126
DB 66 NPESEAVLKAITDEFGVDVNLNAGITRDLILMKRKE-----EKSIDMEINLSIF 119
QY 127 NVIRLVAGENGEPGOGGQGVITNTASVAAFEQGVQAAVSKGCIIVMTLPARD 186
DB 120 RLKSAVILGMMKK-----RGRITIVSGSVGTGMNAGYAAAKAGVIGFTKSMAREV 173
QY 187 APGIRVMTAPGLFPTPLTSLPEKVANFLASQVPPSRIGDPAEVAHLVQALIEP-- 244
DB 174 ASRGVTVAVAPGFIETDMTALNDDEORTATLACVP-AGRLGDEPRLASAV-AFLASPEA 231
QY 245 -FLNGEYIRLDGAI 259
DB 232 AVITGETLHVNGMMV 247

RESULT 19

3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) [imported] - Streptococcus C:Species: Streptococcus pneumoniae
E97919

A:Accession: F86721
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-243 <STO>
A:Cross-references: GB:AE005176; PID:q12723693; PIDN:AAK04872.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: fabG1
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.0%; Score 326.5; DB 2; Length 243;
Best Local Similarity 31.7%; Pred. No. 4.5e-18;
Matches 82; Conservative 48; Mismatches 104; Indels 25; Gaps 6;

QY 8 VAGLVAVITGASGLTAERLVGASAVLLDLPNSGGAOKKL-----GNNQVF 60
DB 3 IKNNVFYVGTGTRIGKALDQFAKAGSNLLI-----NGRSISELLAEFTAGYKAVG 57
QY 61 APADYTSKDYOTALAKGKFRVAVNCAGIYVASKTYNLKKGQTHLEDFQRYLDV 120
DB 58 ISGDISKSEDAKQWAEAEIETLGSVDILVNNAGI--TRDGLSLKMS-----EDFESVLKI 111
QY 121 NIMGTFNVRILVAGENGQNEPDGQGVYINTASVAAPFEGOVGAASASKGGIVGKTL 180
DB 112 NLTGAFNMTOAVL-----KPMTRARSGAIINISSVGLMGNAQANTAAASKAGLIGLTR 165
QY 181 PIARDLAPIGIVMTIAPGLFGPILTLSPKXANFLASQVFPRLGDPAEYAHVQAI 240
DB 166 SIAREYAAKRVNAVNAAPFIESDMTEVLSDKYKNAKMGQIM-KRFGMEPIARATQFL 224
QY 241 IENPFLNGEYIRLDGAIYM 259
DB 225 AEQEVMTGQVLTIDGGVSM 243

RESULT 23
D90481
hypothetical protein fabG-9 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C:Accession: D90481
R:She, Q.; Shing, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Koser, C.J.; Medina, N.C.; Peng, X.; Thi-Ngoc, H.P.; Redder, H.
Submitted to Genbank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: D90481
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-299 <KUR>
A:Cross-references: GB:AE006641; NID:q13816394; PIDN:AAK43107.1; GSPDB:GN00155
C:Genetics:
A:Gene: fabG-9
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 24.3%; Score 317; DB 2; Length 299;
Best Local Similarity 32.5%; Pred. No. 3.2e-17;
Matches 83; Conservative 47; Mismatches 107; Indels 18; Gaps 5;

QY 12 VAVITGASGLTAEERLVGASAVLLDLPNSG---EAQAKKLGNNCVFAPAYTSE 68
DB 4 VSITTGAKGIGAGIAGRLKQGYAVVADYDEAGYRNNHFRGSGISFFTKTIVSSE 63
QY 69 KDVTALALAKGKFRVAVNCAGIYVASKTYNLKKGQTHLEDFQRYLDVNLGTFNV 128
DB 64 MDVSNMVEKYGRGRIDVYVNNAGIGFSKSTI-----EQGITDERRIVETMLTGVMIC 118
QY 129 IRLVAGENGQNEPDGQGVYINTASVAAPFEGOVGAASASKGGIVGKTLPIARDLAP 188
DB 119 SKYAVKYMKNK-----GGVIVINIASTRAFQSEPNTEPYSASKGIIALTSLAVLSLK 171

DB 172 YNIRVYISPGWLDTSRMQVPPRESTLSGLDHQHLTRRVKPKEDVASIVTFVSDASW 231
QY 246 LNGEVIRLDGAIYMQ 260
DB 232 ISGVNFTIDGMATK 246

RESULT 24
H98137
3-oxoacyl-(acyl-carrier protein) reductase (3-ketoacyl-acyl carrier protein reductase
C:Species: Agrobacterium tumefaciens
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C:Accession: H98137
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Gurollo, B.; Goldm
A.; Liu, F.; Mollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
A:Reference number: A97359; PMID:11743194
A:Accession: H98137
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-259 <KUR>
A:Cross-references: GB:AE007870; PIDN:AAK88626.1; PID:q15158345; GSPDB:GN00170
C:Genetics:
A:Gene: AGR_L126
A:Map position: linear chromosome
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 24.3%; Score 316.5; DB 2; Length 259;
Best Local Similarity 36.2%; Pred. No. 2.9e-17;
Matches 94; Conservative 44; Mismatches 91; Indels 31; Gaps 10;

QY 9 KGLVAVITGASGLTAERLVGASAVLLDLPNSGGAOKKLNN-----CYFAP 62
DB 9 KGAVA-ITGASGSGIFSTAOILMARQMPWLLDKRRLDIACKLIGDLMRGIVC--- 63
QY 63 ADVTSKDYOTALAKGKFRVAVNCAGIYVASKTYNLKKGQTHLEDFQRYLDV 118
DB 64 -VDADEASIEAFALPANGADHAYDLVAVVNSGICID-----KLSVDTSEFFRIY 116
QY 119 DVNIMGTFNVRILVAGENGQNEPDGQGVYINTASVAAPFEGOVGAASASKGGIVGK 178
DB 117 DVNIVGSPAVAAARWLESD-----VAGSIVINISSVSGMGRGSAVGSAGVNL 171
QY 179 TLPIARDLAPIGIVMTIAPGLFGPILTLSPKXANFLASQVFPRLGDPAEYAHV 237
DB 172 TMMVAMNELGSGIRVNAIAPGVDTPITQAVHTENVRDQMSRPV-HRYGRMDEIASV 230
QY 238 QAIEN--PFLNGEYIRLDG 255
DB 231 AFLVSDASVINGVLAVDG 250

RESULT 25
A13149
3-oxoacyl-(acyl-carrier protein) reductase [imported] - Agrobacterium tumefaciens (St
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C:Accession: A13149
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo-
erage, G.; Gillet, W.; Grant, C.; Genthner, D.; Kutayian, T.; Levy, R.; Li, M.; MCGI
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kan-
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: A13149
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-259 <KUR>
A:Cross-references: GB:AE008689; PIDN:AA145615.1; PID:q17743336; GSPDB:GN00187

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us-09-931-186-20.rapb

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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:32:58 ; Search time 20.333 Seconds

(without alignments)
1388.950 Million cell updates/sec

Title: US-09-931-186-20

Perfect score: 1304

Sequence: 1 MAACRSYKGLVAVITGAS.....ENPLNGEVIRLDGAIKMP 261

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1304	99.8	261	10	US-09-931-186-20
2	1301	99.7	261	10	US-09-931-186-23
3	1300	99.7	261	10	US-09-931-186-8
4	1299	99.6	261	10	US-09-931-186-2
5	1290	98.9	261	10	US-09-931-186-4
6	1290	98.9	261	10	US-09-931-186-6
7	1137	87.2	227	9	US-09-984-245-245
8	1137	87.2	227	9	US-09-966-262-245
9	1137	87.2	227	9	US-09-983-966-245
10	1137	87.2	227	9	US-09-983-966-245
11	1137	87.2	227	9	US-09-983-966-245
12	1137	87.2	227	9	US-09-983-966-245
13	1137	87.2	227	9	US-09-983-966-245
14	1137	87.2	227	9	US-09-983-966-245
15	1137	87.2	227	9	US-09-983-966-245
16	1137	87.2	227	9	US-09-983-966-245
17	1137	87.2	227	9	US-09-983-966-245
18	1137	87.2	227	9	US-09-983-966-245
19	1137	87.2	227	9	US-09-983-966-245
20	297.5	22.8	267	9	US-09-773-748-1
21	296.5	22.7	262	9	US-10-307-385-6
22	296.5	22.7	262	10	US-09-802-853-6
23	293.5	22.5	270	9	US-09-978-295A-468
24	293.5	22.5	270	9	US-09-978-697-468
25	293.5	22.5	270	9	US-09-978-192A-468
26	293.5	22.5	270	9	US-09-999-832A-468
27	293.5	22.5	270	9	US-09-978-189-468
28	293.5	22.5	270	9	US-09-978-608A-468
29	293.5	22.5	270	9	US-09-978-191A-468
30	293.5	22.5	270	9	US-09-978-403A-468
31	293.5	22.5	270	9	US-09-978-644A-468
32	293.5	22.5	270	9	US-09-978-585A-468
33	293.5	22.5	270	9	US-10-017-081A-468
34	293.5	22.5	270	9	US-09-978-824-468
35	293.5	22.5	270	9	US-09-981-915A-468
36	293.5	22.5	270	9	US-09-999-833A-468
37	293.5	22.5	270	9	US-10-167-749-468
38	293.5	22.5	270	9	US-09-978-585A-468
39	293.5	22.5	270	9	US-09-978-423A-468
40	293.5	22.5	270	9	US-10-013-921A-468
41	293.5	22.5	270	9	US-09-978-193A-468
42	293.5	22.5	270	9	US-10-013-929A-468
43	293.5	22.5	270	9	US-10-016-177A-468
44	293.5	22.5	270	9	US-09-999-830A-468
45	293.5	22.5	270	9	US-09-978-757A-468
46	293.5	22.5	270	9	US-09-978-187A-468
47	293.5	22.5	270	9	US-09-978-643A-468
48	293.5	22.5	270	9	US-10-166-709A-468
49	291.5	22.4	244	10	US-09-815-242-110126
50	288	22.4	263	10	US-09-815-242-14092
51	287.5	22.0	244	9	US-09-849-092-13
52	287.5	22.0	246	9	US-09-364-847-6
53	287.5	22.0	641	9	US-09-364-847-10
54	287.5	22.0	641	9	US-09-364-847-19
55	287.5	22.0	642	9	US-09-364-847-59
56	287.5	22.0	642	9	US-09-364-847-61
57	287.5	22.0	203	9	US-10-175-696-19
58	283.5	21.7	203	10	US-09-823-901-7
59	278	21.3	258	9	US-09-738-626-6436
60	276.5	21.2	286	10	US-09-815-242-11860
61	276	21.2	285	10	US-09-815-242-110241
62	274.5	21.1	254	9	US-09-978-758-2
63	274.5	21.1	272	10	US-09-815-242-12668
64	274	21.0	206	9	US-09-997-816-4
65	273.5	21.0	251	10	US-09-815-242-5689
66	271.5	20.8	246	10	US-09-815-242-5461
67	271.5	20.8	246	10	US-09-815-242-12123
68	271.5	20.8	246	10	US-09-815-242-12803
69	271.5	20.8	246	10	US-09-815-242-13100
70	268.5	20.6	242	10	US-09-815-242-10974
71	268	20.6	251	9	US-10-272-419-20
72	267	20.5	256	10	US-09-954-314-14
73	267	20.5	276	9	US-09-944-160-24
74	266.5	20.4	258	9	US-10-156-055A-1
75	264.5	20.3	252	9	US-09-910-033A-2
76	263	20.2	253	10	US-09-815-242-11842
77	261	20.0	261	9	US-09-971-556-74
78	258	19.8	261	10	US-09-940-037A-29
79	253.5	19.4	266	9	US-09-981-353-40
80	253.5	19.4	266	9	US-09-885-303A-22
81	253.5	19.4	266	9	US-10-205-823-176
82	253.5	19.4	266	10	US-09-931-186-18
83	249	19.1	221	10	US-09-764-853-553
84	246.5	18.9	261	10	US-09-815-242-10846
85	246.5	18.9	262	10	US-09-815-242-10597
86	242	18.6	255	10	US-09-931-186-14
87	241	18.5	251	10	US-09-922-001-16
88	240	18.4	247	10	US-09-815-242-11893
89	240	18.4	258	10	US-09-954-314-12
90	239.5	18.4	274	9	US-09-976-059-17
91	236	18.1	271	9	US-09-815-242-13987
92	236	18.1	272	10	US-09-815-242-13679

93 235 18.0 311 9 US-09-738-626-3819 Sequence 3819, Ap
94 231 17.7 261 10 US-09-815-242-5613 Sequence 5813, Ap
95 227.5 17.4 247 10 US-09-815-242-11342 Sequence 11342, A
96 227 17.4 254 10 US-09-741-669-411 Sequence 411, App
97 224.5 17.2 247 10 US-09-815-242-11514 Sequence 11514, A
98 222.5 17.1 900 9 US-10-060-230-15 Sequence 15, App1
99 222.5 17.1 900 9 US-10-060-230-17 Sequence 17, App1
100 218.5 16.8 253 10 US-09-815-242-10279 Sequence 10279, A

ALIGNMENTS

RESULT 1

US-09-931-186-20 Application US/09931186
Sequence 20, Application US/09931186
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABREO, MELWYN A.
APPLICANT: AGRE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REUTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPCZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 261
TYPE: PRP
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C214A
US-09-931-186-20

Query Match 100.0%; Score 1304; DB 10; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.8e-109;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACRSYKGLVAVITGASGLGATATRLVGGASAVLLDLPNSGGAQAKLGNCF 60
DB 1 MAACRSYKGLVAVITGASGLGATATRLVGGASAVLLDLPNSGGAQAKLGNCF 60
QY 61 APADVTSEKDVOTATLAKKFRVDVAVNCAGIAVASKTYNLKKGOTHTLEDFOVRLDV 120
DB 61 APADVTSEKDVOTATLAKKFRVDVAVNCAGIAVASKTYNLKKGOTHTLEDFOVRLDV 120
QY 121 NMGTENVIRLVAGEMGQNEPDGQGRVYIINTASVAAFEGOVGAAYASAKGIGVMTL 180
DB 121 NMGTENVIRLVAGEMGQNEPDGQGRVYIINTASVAAFEGOVGAAYASAKGIGVMTL 180
QY 181 PIARDLAPIGIRVMTIAGLFTPLTSLPEKXANFLASQVPPSRIGDPAEYAHVQAI 240
DB 181 PIARDLAPIGIRVMTIAGLFTPLTSLPEKXANFLASQVPPSRIGDPAEYAHVQAI 240
QY 241 IENPFLNGEVIIRLDGAIKMP 261
DB 241 IENPFLNGEVIIRLDGAIKMP 261

US-09-931-186-23

Sequence 23, Application US/09931186
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABREO, MELWYN A.
APPLICANT: AGRE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REUTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPCZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 261
TYPE: PRP
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C214S
US-09-931-186-23

Query Match 99.8%; Score 1301; DB 10; Length 261;
Best Local Similarity 99.6%; Pred. No. 3.4e-109;
Matches 260; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACRSYKGLVAVITGASGLGATATRLVGGASAVLLDLPNSGGAQAKLGNCF 60
DB 1 MAACRSYKGLVAVITGASGLGATATRLVGGASAVLLDLPNSGGAQAKLGNCF 60
QY 61 APADVTSEKDVOTATLAKKFRVDVAVNCAGIAVASKTYNLKKGOTHTLEDFOVRLDV 120
DB 61 APADVTSEKDVOTATLAKKFRVDVAVNCAGIAVASKTYNLKKGOTHTLEDFOVRLDV 120
QY 121 NMGTENVIRLVAGEMGQNEPDGQGRVYIINTASVAAFEGOVGAAYASAKGIGVMTL 180
DB 121 NMGTENVIRLVAGEMGQNEPDGQGRVYIINTASVAAFEGOVGAAYASAKGIGVMTL 180
QY 181 PIARDLAPIGIRVMTIAGLFTPLTSLPEKXANFLASQVPPSRIGDPAEYAHVQAI 240
DB 181 PIARDLAPIGIRVMTIAGLFTPLTSLPEKXANFLASQVPPSRIGDPAEYAHVQAI 240
QY 241 IENPFLNGEVIIRLDGAIKMP 261
DB 241 IENPFLNGEVIIRLDGAIKMP 261

RESULT 3

US-09-931-186-8
Sequence 8, Application US/09931186
Patent No. US20020132319A1

GENERAL INFORMATION:
APPLICANT: ABREO, MELWYN A.
APPLICANT: AGRE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REUTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.

APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: wild type ERAB
US-09-931-186-8

Query Match 99.7%; Score 1300; DB 10; Length 261;
Best Local Similarity 99.6%; Pred. No. 4,2e-109;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAACRSYKGLVAVITGASGLGATAEPLVGGASAVLLDLPNSGGEQAQAKKLGNCVF 60
DB 1 MAACRSYKGLVAVITGASGLGATAEPLVGGASAVLLDLPNSGGEQAQAKKLGNCVF 60
QY 61 APADVTSEKDYQATLALAKGKFGKRVDAVNCAGIAVASKTYNKKGGTHTLEDFQRYLDV 120
DB 61 APADVTSEKDYQATLALAKGKFGKRVDAVNCAGIAVASKTYNKKGGTHTLEDFQRYLDV 120
QY 121 NLMGTFNVIRLVAGEMQNEPDQGGQGVIIINTASVAAFEGQVQAAYSASKGIYGMTL 180
DB 121 NLMGTFNVIRLVAGEMQNEPDQGGQGVIIINTASVAAFEGQVQAAYSASKGIYGMTL 180
QY 181 PIARDLAPIGIRVMTAPGLFTGTPLLTSLEKYNFNLASQVFPFSLRGDPAEYAHLYQAI 240
DB 181 PIARDLAPIGIRVMTAPGLFTGTPLLTSLEKYNFNLASQVFPFSLRGDPAEYAHLYQAI 240
QY 241 IENPFLNGEVIIRLDGAIRMOP 261
DB 241 IENPFLNGEVIIRLDGAIRMOP 261

RESULT 4
US-09-931-186-2
Sequence 2, Application US/09931186
Patent No. US20020132319A1

GENERAL INFORMATION:
APPLICANT: ABREO, MELWYN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPCZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 261
TYPE: PRT

ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C214R
US-09-931-186-2

Query Match 99.6%; Score 1299; DB 10; Length 261;
Best Local Similarity 99.6%; Pred. No. 5,1e-109;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAACRSYKGLVAVITGASGLGATAEPLVGGASAVLLDLPNSGGEQAQAKKLGNCVF 60
DB 1 MAACRSYKGLVAVITGASGLGATAEPLVGGASAVLLDLPNSGGEQAQAKKLGNCVF 60
QY 61 APADVTSEKDYQATLALAKGKFGKRVDAVNCAGIAVASKTYNKKGGTHTLEDFQRYLDV 120
DB 61 APADVTSEKDYQATLALAKGKFGKRVDAVNCAGIAVASKTYNKKGGTHTLEDFQRYLDV 120
QY 121 NLMGTFNVIRLVAGEMQNEPDQGGQGVIIINTASVAAFEGQVQAAYSASKGIYGMTL 180
DB 121 NLMGTFNVIRLVAGEMQNEPDQGGQGVIIINTASVAAFEGQVQAAYSASKGIYGMTL 180
QY 181 PIARDLAPIGIRVMTAPGLFTGTPLLTSLEKYNFNLASQVFPFSLRGDPAEYAHLYQAI 240
DB 181 PIARDLAPIGIRVMTAPGLFTGTPLLTSLEKYNFNLASQVFPFSLRGDPAEYAHLYQAI 240
QY 241 IENPFLNGEVIIRLDGAIRMOP 261
DB 241 IENPFLNGEVIIRLDGAIRMOP 261

RESULT 5
US-09-931-186-4
Sequence 4, Application US/09931186
Patent No. US20020132319A1

GENERAL INFORMATION:

APPLICANT: ABREO, MELWYN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPCZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C5V
US-09-931-186-4

Query Match 98.9%; Score 1290; DB 10; Length 261;
Best Local Similarity 99.2%; Pred. No. 3,3e-108;
Matches 259; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAACRSYKGLVAVITGASGLGATAEPLVGGASAVLLDLPNSGGEQAQAKKLGNCVF 60
DB 1 MAACRSYKGLVAVITGASGLGATAEPLVGGASAVLLDLPNSGGEQAQAKKLGNCVF 60
QY 61 APADVTSEKDYQATLALAKGKFGKRVDAVNCAGIAVASKTYNKKGGTHTLEDFQRYLDV 120
DB 61 APADVTSEKDYQATLALAKGKFGKRVDAVNCAGIAVASKTYNKKGGTHTLEDFQRYLDV 120
QY 121 NLMGTFNVIRLVAGEMQNEPDQGGQGVIIINTASVAAFEGQVQAAYSASKGIYGMTL 180
DB 121 NLMGTFNVIRLVAGEMQNEPDQGGQGVIIINTASVAAFEGQVQAAYSASKGIYGMTL 180
QY 181 PIARDLAPIGIRVMTAPGLFTGTPLLTSLEKYNFNLASQVFPFSLRGDPAEYAHLYQAI 240
DB 181 PIARDLAPIGIRVMTAPGLFTGTPLLTSLEKYNFNLASQVFPFSLRGDPAEYAHLYQAI 240
QY 241 IENPFLNGEVIIRLDGAIRMOP 261
DB 241 IENPFLNGEVIIRLDGAIRMOP 261

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Db 61 APADVTSEKDVQATALALAKGFGVDVAVNCAGIAVASKTYNLIKKGQHTLEDFORVLDV 120
QY 121 NLMGTFNVIRLYAGGEGNEPQGGQRCYITNTASVAAREGVGQAASASKGIWMTL 180
Db 121 NLMGTFNVIRLYAGGEGNEPQGGQRCYITNTASVAAREGVGQAASASKGIWMTL 180
QY 181 PIARDLAPIGIRMTIAPGLFCTPLTSLPERKVFASQVFPSPRLGDPATYAHLYQAI 240
Db 181 PIARDLAPIGIRMTIAPGLFCTPLTSLPERKVFASQVFPSPRLGDPATYAHLYQAI 240
QY 241 IENPFLNGEYIRLDGAIRMOP 261
Db 241 IENPFLNGEYIRLDGAIRMOP 261
```

RESULT 6

```
US-09-931-186-6
Sequence 6, Application US/09931186
Patent No. US2002013219A1
GENERAL INFORMATION:
APPLICANT: ABERO, MELVYN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAC, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOMALTER, RICHARD E.
APPLICANT: TEMPCEYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLARANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADR2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 6
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C56V
US-09-931-186-6
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Query Match 98.9%; Score 1290; DB 10; Length 261;
Best Local Similarity 99.2%; Pred. No. 3.3e-108;
Matches 259; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 MAACRSYKGIIVAVITGASGLGATPERLVGGASAVLLDLSNGSGEAAKXKLGNNCYF 60
Db 1 MAACRSYKGIIVAVITGASGLGATPERLVGGASAVLLDLSNGSGEAAKXKLGNNCYF 60
QY 61 APADVTSEKDVQATALALAKGFGVDVAVNCAGIAVASKTYNLIKKGQHTLEDFORVLDV 120
Db 61 APADVTSEKDVQATALALAKGFGVDVAVNCAGIAVASKTYNLIKKGQHTLEDFORVLDV 120
QY 121 NLMGTFNVIRLYAGGEGNEPQGGQRCYITNTASVAAREGVGQAASASKGIWMTL 180
Db 121 NLMGTFNVIRLYAGGEGNEPQGGQRCYITNTASVAAREGVGQAASASKGIWMTL 180
QY 181 PIARDLAPIGIRMTIAPGLFCTPLTSLPERKVFASQVFPSPRLGDPATYAHLYQAI 240
Db 181 PIARDLAPIGIRMTIAPGLFCTPLTSLPERKVFASQVFPSPRLGDPATYAHLYQAI 240
QY 241 IENPFLNGEYIRLDGAIRMOP 261
Db 241 IENPFLNGEYIRLDGAIRMOP 261
```

RESULT 7

```
US-09-984-245-245
Sequence 245, Application US/09984245
Patent No. US2002016537A1
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: P2004P1
CURRENT APPLICATION NUMBER: US/09/984,245
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 09/154,707
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: PCT/US98/05311
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: US 60/041,277
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/042,344
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/041,276
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/041,281
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/048,094
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,350
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,188
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,135
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/050,937
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,187
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,099
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,352
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,186
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,069
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,095
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,131
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,096
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,355
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,160
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/056,370
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: US 60/060,862
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 343
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 245
LENGTH: 227
TYPE: PRT
ORGANISM: Homo sapiens
US-09-984-245-245
```

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Query Match 87.2%; Score 1137; DB 9; Length 227;
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Thu Jun 26 06:55:04 2003

us-09-931-186-20.rapb

Page 5

Best Local Similarity 99.6%; Pred. No. 1.5e-94;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 35 ASAVLLDLPNSGGEAOKKLNCCVAFAPADVTSEKDVOTATLAKGKFGVDVAVNCAGI 94
DB 1 ASAVLLDLPNSGGEAOKKLNCCVAFAPADVTSEKDVOTATLAKGKFGVDVAVNCAGI 60
QY 95 AVASTYNNLKKGGQHTLLEDFQRLVDVNLMTGFNVIRLVAGMGONEPDGGQGRVYIINTA 154
DB 61 AVASTYNNLKKGGQHTLLEDFQRLVDVNLMTGFNVIRLVAGMGONEPDGGQGRVYIINTA 120
QY 155 SVAAFEGVGOAAYASASKSGIVGKTLPIARDLAPIGIRVMTIAPGLFGTPIILTSLEPKYA 214
DB 121 SVAAFEGVGOAAYASASKSGIVGKTLPIARDLAPIGIRVMTIAPGLFGTPIILTSLEPKYC 180
QY 215 NFLASQVFPSPSRIGDPAEYAHLYQAIIENPFLNGEYIRLDGAIRMOP 261
DB 181 NFLASQVFPSPSRIGDPAEYAHLYQAIIENPFLNGEYIRLDGAIRMOP 227

RESULT 8
US-09-966-262-245
; Sequence 245, Application US/09966262
; Publication No. US20030050461A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/966,262
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: US 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351

PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 245
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-966-262-245

Query Match 87.2%; Score 1137; DB 9; Length 227;
Best Local Similarity 99.6%; Pred. No. 1.5e-94;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 35 ASAVLLDLPNSGGEAOKKLNCCVAFAPADVTSEKDVOTATLAKGKFGVDVAVNCAGI 94
DB 1 ASAVLLDLPNSGGEAOKKLNCCVAFAPADVTSEKDVOTATLAKGKFGVDVAVNCAGI 60
QY 95 AVASTYNNLKKGGQHTLLEDFQRLVDVNLMTGFNVIRLVAGMGONEPDGGQGRVYIINTA 154
DB 61 AVASTYNNLKKGGQHTLLEDFQRLVDVNLMTGFNVIRLVAGMGONEPDGGQGRVYIINTA 120
QY 155 SVAAFEGVGOAAYASASKSGIVGKTLPIARDLAPIGIRVMTIAPGLFGTPIILTSLEPKYA 214
DB 121 SVAAFEGVGOAAYASASKSGIVGKTLPIARDLAPIGIRVMTIAPGLFGTPIILTSLEPKYC 180
QY 215 NFLASQVFPSPSRIGDPAEYAHLYQAIIENPFLNGEYIRLDGAIRMOP 261
DB 181 NFLASQVFPSPSRIGDPAEYAHLYQAIIENPFLNGEYIRLDGAIRMOP 227

RESULT 9
US-09-983-966-245
; Sequence 245, Application US/09983966
; Publication No. US20030060619A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/983,966
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099

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;; ORGANISM: Homo sapiens
US-10-143-090-245
Query Match
Best Local Similarity 87.2%; Score 1137; DB 9; Length 227;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,352
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,186
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,069
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,095
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,131
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,096
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,355
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,160
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,351
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,154
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/054,804
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: US 60/056,370
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: US 60/060,862
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 343
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 245
LENGTH: 227
TYPE: PRT
ORGANISM: Homo sapiens
US-09-963-966-245
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Query Match
Best Local Similarity 87.2%; Score 1137; DB 9; Length 227;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

35 ASAYLLDLPNSGGGAQAKKLNCCVFPADYTSKDVOTLALAKKFGRYDAVNCAGI 94
|||||
1 ASAYLLDLPNSGGGAQAKKLNCCVFPADYTSKDVOTLALAKKFGRYDAVNCAGI 60
|||||

95 AVASKTYNLKKGGQHTLEDFORVLDVNLKGTFFNVIRLVAGEMQNEPDGGQGRVLIINTA 154
|||||
61 AVASKTYNLKKGGQHTLEDFORVLDVNLKGTFFNVIRLVAGEMQNEPDGGQGRVLIINTA 120
|||||

155 SVAAFEQGVQQAAYSASAKSGIVGWTLPARDLAPIGIRVMTIAPGLFTPLTSLPERKVA 214
|||||
121 SVAAFEQGVQQAAYSASAKSGIVGWTLPARDLAPIGIRVMTIAPGLFTPLTSLPERKVC 180
|||||

215 NFLASQVFPSPRLGDPAPAYAHVQAIIENPFLNGEVIRLDGAIRMP 261
|||||
181 NFLASQVFPSPRLGDPAPAYAHVQAIIENPFLNGEVIRLDGAIRMP 227
|||||

RESULT 10
US-10-143-090-245
Sequence 245, Application US/10143090
Publication No. US20030069406A1
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: P2004P1
CURRENT APPLICATION NUMBER: US/10/143,090
CURRENT FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: 09/154,707
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 343
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 245
LENGTH: 227
TYPE: PRT
```

```
;; ORGANISM: Homo sapiens
US-10-143-090-245
Query Match
Best Local Similarity 87.2%; Score 1137; DB 9; Length 227;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

35 ASAYLLDLPNSGGGAQAKKLNCCVFPADYTSKDVOTLALAKKFGRYDAVNCAGI 94
|||||
1 ASAYLLDLPNSGGGAQAKKLNCCVFPADYTSKDVOTLALAKKFGRYDAVNCAGI 60
|||||

95 AVASKTYNLKKGGQHTLEDFORVLDVNLKGTFFNVIRLVAGEMQNEPDGGQGRVLIINTA 154
|||||
61 AVASKTYNLKKGGQHTLEDFORVLDVNLKGTFFNVIRLVAGEMQNEPDGGQGRVLIINTA 120
|||||

155 SVAAFEQGVQQAAYSASAKSGIVGWTLPARDLAPIGIRVMTIAPGLFTPLTSLPERKVA 214
|||||
121 SVAAFEQGVQQAAYSASAKSGIVGWTLPARDLAPIGIRVMTIAPGLFTPLTSLPERKVC 180
|||||

215 NFLASQVFPSPRLGDPAPAYAHVQAIIENPFLNGEVIRLDGAIRMP 261
|||||
181 NFLASQVFPSPRLGDPAPAYAHVQAIIENPFLNGEVIRLDGAIRMP 227
|||||
```

```
RESULT 11
US-09-920-923-41
Sequence 41, Application US/09920923
Publication No. US20030022273A1
GENERAL INFORMATION:
APPLICANT: Pasamontes, Luis
APPLICANT: Tszyankov, Yuri
TITLE OF INVENTION: Improved Fermentative Carotenoid Production
FILE REFERENCE: Improved Fermentative Carotenoid
CURRENT APPLICATION NUMBER: US/09/920,923
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 08/980,832
PRIOR FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 41
LENGTH: 388
TYPE: PRT
ORGANISM: Flavobacterium sp. RJ534
US-09-920-923-41

Query Match
Best Local Similarity 51.1%; Score 666.5; DB 9; Length 388;
Matches 141; Conservative 35; Mismatches 69; Indels 9; Gaps 3;

8 VKGIVAVITGSGSGIGLTAERLVQGGASVYLLDLPNSGGGAQAKKLNCCVFPADYTS 67
|||||
143 IGRVFFVVTGAASGGAASARMLAOGGAKVVIADL-----AEPRDADEGAVHAAQDVTD 196
|||||
68 EKDVOTLALAKKFGRYDAVNCAGIYVASKTYNLKKGGQHTLEDFORVLDVNLKGTFF 127
|||||
197 ATAAQGTALATDRGRDLGVLNCCAGIAPAEEM--LGRDGPRIQDLSFRAVATINLIGSFN 254
|||||

128 VIRLVAGEMQNEPDGGQGRVLIINTASVAAFEQGVQQAAYSASAKSGIVGWTLPARDLA 187
|||||
255 MARLAEAARARNEPR-GERGVIVTASTIAAQDQIGVVAASAGVAGMTLPPARDLA 313
|||||
188 PIGIRVMTIAPGLFTPLTSLPERKVAIIENPFLNGEVIRLDGAIRMP 247
|||||
314 RIGIRVMTIAPGLFTPLTSLPERKVAIIENPFLNGEVIRLDGAIRMP 373
|||||

248 GEVIRLDGAIRMP 261
|||||
374 GEVIRLDGAIRMP 387
|||||

RESULT 12
US-09-931-186-17
Sequence 17, Application US/09931186
```

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```
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: AGREE, MELWYN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPCZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-06-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 259
TYPE: PRT
ORGANISM: Homo sapiens
US-09-931-186-17
```

```
Query Match      25.6%; Score 333.5; DB 10; Length 259;
Best Local Similarity 31.2%; Pred. No. 2.8e-22;
Matches 83; Conservative 51; Mismatches 105; Indels 27; Gaps 7;
```

```
QY 8 VKGLVAVITGGASGLTAEIRLVGQASAVLLDLPNSGGEAOKKL-----GN 56
DB 7 LRSALALVITGGASGLTAEIRLVGQASAVLLDLPNSGGEAOKKL-----GN 56
QY 57 NCVFPAADVTSKEDVOTALAKGKFR-VDVAVNCAGIAVASKTYNKKQCTHTLEDFQ 115
DB 67 HNAF-QADVSEARARCLLEVOACFSRPPSVVASCAGITQDEFLHSE-----DDWD 119
QY 116 RLVDAVNLKGTFTVTLVAGEMQNEPDDGQGVIIINTASVAEFEGOVGAAYASASKGI 175
DB 120 KYIAVNLKGTFTVTLVAGEMQNEPDDGQGVIIINTASVAEFEGOVGAAYASASKGI 174
QY 176 VGMTPIARDLAPIGIRVNTIAPGLTGLTSLTPEKVANFLASQVPPSRIGDPAEYAH 235
DB 175 IGLTGTAARELGRHGRCSVLPGLIATPMQKVPQKVDKITEMIPM-GHLGDPEVDAD 233
QY 236 LVQ--AIENPFLNGEVRIRLDAIKM 259
DB 234 VVAFLASEDSGYITGTSTVEVTGLPM 259
```

```
RESULT 13
US-09-815-242-13360
Sequence 13360, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
```

```
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 1410
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13360
LENGTH: 243
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-815-242-13360
```

```
Query Match      25.2%; Score 328.5; DB 10; Length 243;
Best Local Similarity 35.1%; Pred. No. 7.3e-22;
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;
```

```
QY 15 ITGASGLTAEIRLVGQASAVLLDLPNSGGE-----AQAKLGNVCVPAADVISE 68
DB 10 ITGSSRGIGLAIHAKRAQAGANIVL-----NSRGALISELLAEFSNYGIKVPISGDVDF 65
QY 69 KDVOFLALAKGFGKRDVAVNCAGIAVASKTYNKKQCTHTLEDFQVRLDPAEYAH 128
DB 66 ADKRMIDQAIYALGSDVAVNNAGI--TQDTMLKK---TDADEKVLKVLTAQFMK 119
QY 129 IRVAGEMQNEPDDGQGVIIINTASVAEFEGOVGAAYASASKGIIVGMTPIARDLAP 188
DB 120 TQSVL-----KPMKMRREGAIITMSVVGIMGNIGANVAASKAGLIGFTKSVAREVAS 173
QY 189 IGRVNTIAPGLTGLTSLTPEKVANFLASQVPPSRIGDPAEYAHVIAIENPFLNG 248
DB 174 RNIKRVNTIAPGMTESDMTALISDKIKETLAQIIPM-KEFGQADQVADLTVELAGQDYLTS 232
QY 249 EVIRLDGAIKM 259
DB 233 QVIAIDGSLM 243
```

```
RESULT 14
US-09-815-242-13581
Sequence 13581, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
```


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RESULT 17
US-09-823-901-2
: Sequence 2, Application US/09823901
: Patent No. US20020001807A1
: GENERAL INFORMATION:
: APPLICANT: Meyers, Rachel
: TITLE OF INVENTION: 21509 AND 33770. NOVEL HUMAN
: TITLE OF INVENTION: DEHYDROGENASES AND USES THEREOF
: FILE REFERENCE: 1048-036001
: CURRENT APPLICATION NUMBER: US/09/823,901
: CURRENT FILING DATE: 2001-03-30
: PRIOR APPLICATION NUMBER: US 60/193,920
: PRIOR FILING DATE: 2000-03-31
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO. 2
: LENGTH: 237
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-823-901-2

```

Query Match	32.1%	Score 314;	DB 10;	Length 237;
Best Local Similarity	32.0%	Pred. No. 1,4e-20;		
Matches	81;	Conservative	41;	Mismatches 105; Indels 26; Gaps 5
QY	12	VAVTGGASGCLAAERLVGGASAVLIDLENSGGEQAKKLGNNCFAPADVTSKDY	71	
DB	4	VCATGGSGGICRAVAQIMARKGRPLAIARNLEAKAAAGLDGDHAFSCDAKEHY	63	
QY	72	QTALALAKGKFEGRVVAVACAGI-----AVASKTYNLKKQTHTEDEFGVLDVLMGTF	126	
DB	64	QWTFEMEKHLGRVNFVFLVMAAGINDRSLVTRKT-----EDWVSLQHTNLLGSM	112	
QY	127	NVIRLVAGEMGNEEDQGGQRCVITINTASVAFBEQVQGAASAKSGIVGVTLLIARL	186	
DB	113	LTCKAMRAMIQO-----QGSIVNVGSLVGLKNGSGSVYSASRKGVLVGRSLAKAV	166	
QY	187	AFIGIRVMIAIDEGTPLLITSLPERKANFLLASQVFPFSRLDPAPAEVALVQAIINENPL	246	
DB	167	ARKKIRVVNVAVAGFVHTDKDLKEE--HKKNIPL-GRGSETIEVAHAVVFLLESPTI	222	
QY	247	NGEVIRLDGAIKM	259	
DB	223	TGHVLLVVDGGLQI	235	

RESULT 18
US-09-931-186-15
Sequence 15 Application US/09931186

```

Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABREO, MELWYN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAR, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOMALTER, RICHARD E.
APPLICANT: TEMPCZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLARANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
TITLE OF INVENTION: OF INHIBITORS THEREOF
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 253
TYPE: PRT
ORGANISM: Steptomyces hydrogenans
US-09-931-186-15

```

Query Match	23.7%	Score 308.5	DB 10	Length 253
Best Local Similarity	33.3%	Pred. No. 4,8e-20		
Matches	84	Conservative	48	Mismatches 101; Indels 19; Gaps 7;
Qy	8	VKGLVAVITGASGIGLTAETRLVGQGSAYALLDIPNSGEPQAKKGINCVFAPADYTS	67	
		Match:		
Db	3	LSGRTVITLTGARGIGASAEAAQAAVAGARVVLADLDEGAATARELDDAARYOHLDTI	62	
		Match:		
Qy	68	EKDVTOTALAKKKGKGRVDVAVNCAGIVASKTYLKKGQHTLEDFORVLDVNMIGTFN	127	
		Match:		
Db	63	EDDMQRYAVAYAREEGSVDLGNNAIGITGMFL-----ETESYERFRKYVEINLTGVEI	116	
		Match:		
Qy	128	VIRLVAGMGONPEPDGGQRGVYIINTASVAAFEQGVQGAASASASGGIVGMTLPIAROLA	187	
		Match:		
Db	117	GKRTVTPAM---KAGG--GSIVNISSAAGLGMALTSSYGASKSWYGRGSKLAIVELG	170	
		Match:		
Qy	188	PIGIRVMKIADGLFQTPLL--TSLDEKXANFLASQVPPPSRLQGPAAEYAHVLQALIE--N	243	
		Match:		
Db	171	TDRIRVNSVHDMGTPTPTAETGIRQGGN--PMTPM-GRVGEPEGIAGAVVKLLSDTS	227	
		Match:		
Qy	244	PFLNGEVRRLDG	255	
		Match:		
Db	228	SVYTGAEIADVQ	239	

```

/ RESULT 19
/ US-09-479-040-9
/ Sequence 9, Application US/09479040
/ Publication No. US20020182690A1
/ GENERAL INFORMATION:
/ APPLICANT: Mccool, Gabriel J.
/ APPLICANT: Cannon, Maura C.
/ APPLICANT: Cannon, Francis C.
/ APPLICANT: Valentin, Henry E.
/ APPLICANT: Guze, Kenneth J.
/ TITLE OF INVENTION: POLYHYDROXYALKANOATE BIOSYNTHESIS ASSOCIATED PROTEINS
/ TITLE OF INVENTION: AND CODING REGION IN BACILLUS MEGATERIUM
/ FILE REFERENCE: M087212
/ CURRENT APPLICATION NUMBER: US/09/479,040
/ NUMBER OF SEQ ID NOS: 29
/ CURRENT FILING DATE: 2000-01-07
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 9
/ LENGTH: 247

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TYPE: PR
ORGANISM: Bacillus megaterium
US-09-479-040-9

Query Match 23.2%; Score 303; DB 9; Length 247;
Best Local Similarity 29.1%; Pred. No. 1.5e-19;
Matches 78; Conservative 59; Mismatches 93; Indels 38; Gaps 9;

QY 7 SVAGLVAVITGASGGLATAEELVQG-----ASAVLLDLPNNGSGGAQAK 53
DB 3 TLGGKVAIVGSGKGGALTRRELASNGKVAAYNNSSKESAEATVKEIKDNGGA---- 58
QY 54 LGNNCFAPADVTSEKDVOTALAKGKGRVDVAVNCAGIAVASKTYNLRK-GQTHTLE 112
DB 59 -----TAVQADVSYDQAKHLIETKAARGQDLIVNNGI---TRDRSFKLGE-----E 106
QY 113 DEQVLDVNLMTGPNVIRLVAGEMQNEPDGQGRVYINTASVALEEGVQGAASAK 172
DB 107 DMKRVIDVNLHSYNTTSAALTRLESE---GGR---VINISSIQAGGFGQTNISAK 160
QY 173 GGIYGTLPFARDLAPGIRVMTIAPGLFTPLLSPEKVAFLASQVPPFSRLGDPAE 232
DB 161 AGHLGFTKSLALELAKTGVVNAICPGFITEEMVMAIPEDVRKIKYAKIP-TRRLGHAE 219
QY 233 YAH-LVQAITENPPLNGEVIRLDGAIRM 259
DB 220 IARGVVIADKGAVITGQOLNIGLIYM 247

RESULT 20
US-09-773-748-1
Sequence 1, Application US/09773748
Publication No. US20020187537A1
GENERAL INFORMATION:
APPLICANT: Wada, Masaru
TITLE OF INVENTION: Levodione reductase gene and use thereof
FILE REFERENCE: Levodione reductase
CURRENT APPLICATION NUMBER: US/09/773,748
CURRENT FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: EP00101665.8
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 267
TYPE: PR
ORGANISM: Corynebacterium aquaticum
US-09-773-748-1

Query Match 22.8%; Score 297.5; DB 9; Length 267;
Best Local Similarity 32.2%; Pred. No. 5.1e-19;
Matches 85; Conservative 45; Mismatches 97; Indels 37; Gaps 9;

RESULT 21
US-10-307-385-6
Sequence 6, Application US/10307385
Publication No. US20030077797A1
GENERAL INFORMATION:
APPLICANT: SUGIYAMA, MASAKAZU
APPLICANT: TONOUCHI, NAOTO
APPLICANT: SUZUKI, SHUNICHI
APPLICANT: YOKOZAKI, KENZO
TITLE OF INVENTION: XYLTOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF
FILE REFERENCE: 0010-1024-0
CURRENT APPLICATION NUMBER: US/10/307,385
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: US/09/363,189
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: JP10-216047
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 262
TYPE: PR
ORGANISM: Gluconobacter oxydans
US-10-307-385-6

Query Match 22.7%; Score 296.5; DB 9; Length 262;
Best Local Similarity 32.0%; Pred. No. 6.1e-19;
Matches 87; Conservative 41; Mismatches 109; Indels 35; Gaps 7;

QY 6 RSVKGLVAVITGASGGLATAEELVQGASAVLLDLPNSG---GEAQAARKLNNCFAP 62
DB 3 KRFNGKVLIVTQAGNIGLTLRLAEGTALILDMRELKAEAVRREKVEARVY 62
QY 63 ADVTSEKDVOTALAKGKGRVDVAVNCAGIAVASKTYNLRK-GQTHTLEDFORVLDVNL 122
DB 63 CVTSEBNAVITGVDSVDRDFGKIDELFNNAQOGA-----FAPVDYPSDDFAVRLTIV 117
QY 122 MGFENVIRLVAGEM-GONEPDGQGRVYINTASVALEEGVQGAASAKSGGIYGTLP 181
DB 118 TCAFHYLKVSKOMITON-----YGRVMTASAGVKGPPNNMAYGASGAILTLET 170
QY 182 IARDLAPGIRVMTIAPGLF-----GIPLTLSPEKVAFLASQVPPFS 225
DB 171 AALDLAPYINIRVNAISPFGMPFMEQVLEQAKVGSQYSTDKRVAAQMGISVPM-R 229
QY 226 RLGDDPAEYVLAHVOAIT--ENPPLNGEVIRLDG 255
DB 230 RYGDINEIPGVVAFLLGDDSSPMTCVNLPIAG 261

RESULT 22
US-09-802-853-6
Sequence 6, Application US/09802853
Patent No. US20010034049A1
GENERAL INFORMATION:
APPLICANT: SUGIYAMA, MASAKAZU
APPLICANT: TONOUCHI, NAOTO
APPLICANT: SUZUKI, SHUNICHI
APPLICANT: YOKOZAKI, KENZO
TITLE OF INVENTION: XYLTOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF
FILE REFERENCE: 0010-1024-0
CURRENT APPLICATION NUMBER: US/09/802,853
CURRENT FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 09/363,189
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: JP10-216047
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 262
TYPE: PR

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ORGANISM: Gluconobacter oxydans
us-09-802-853-6

Query Match 22.7%; Score 296.5; DB 10; Length 262;
Best Local Similarity 32.0%; Pred. No. 6,1e-19;
Matches 87; Conservative 41; Mismatches 109; Indels 35; Gaps 7;

QY 6 RSVKGLVAVITGGASGLIATIERLVGGASAVLIDPNSG---GEOAKLGNKCYFAP 62
DB 3 KKFNGKVLTVGAGNGIGIATLRLAEGTIALIDMNRALERKASRVEARSYV 62
QY 63 ADVSEKDVOTALALAKFGFVDVAACAGIAVASKTYNKKGQTHLEDFORVLDVNL 122
DB 63 CVTSEAVITGVDSVDFEKTIDLFNNAGYGA-----TAPVDYPSDDFARVLTINV 117
QY 123 MGFENVIRLVGEM-GQNEPDGGGQGVITINTASYAATGQVGAAYASAKGIVGMLP 181
DB 118 TGAFFVLKAVSRKMTTON-----YGRIVTVASMAVGKGPNNMAAGASGAILTET 170
QY 182 IARDLAPIGIRVMTIAPGLF-----GPILTSLPEKAVNLAASGVPPS 225
DB 171 AALDLAPVIRVNAISPFGMGPFMERQVELQAKVSGQYFTDPKVVAAQDMISVPM-R 229
QY 226 RLGDPAEYAHVQAIT--ENPLNGEVRILDG 255
DB 230 RYGDINEIPGVAFILGDDSSFMGTGNLPJAG 261

RESULT 23
US-09-978-295A-468
Sequence 468, Application US/09978295A
Patent No. US2002015606A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
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PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819

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      PRIOR FILING DATE: 1998-05-15
      PRIOR APPLICATION NUMBER: 60/085697

Query Match      22.5%; Score 293.5; DB 9; Length 270;
Best Local Similarity 32.7%; Pred. No. 1.2e-18;
Matches 86; Conservative 42; Mismatches 114; Indels 21; Gaps 8

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Db      1 MATGR-VAGKVVVVTGGGRGIGAGIVAFVNSGARVVICXKDSGGRALQEL-PCAYF 58
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Db      59 ILCDVTEEDVTVLSETIRRGRLDCVNNAGHPP-----QRPETSHQGRLEL 113
OY      121 NLMGTFNVLVAGHEGQNEPDGQGRGVIIINTASVAFAEQVGOAAYSASKGIVGTL 180
Db      114 NLGTVTLKRLAPLTKRSQ-----GNVINSISLVGAIGQAQAVPVYATKGAVTMTK 166
OY      161 PIRADLPAGIRVMTIAPGLFETPLTSL---PEKVNFIASGVPP-SRLGPPAY-A 234
Db      167 ALALDSSPGVARNCSIPENITPILMEELALMPDPRAITREGHLAQPLGRMQPALVGA 226
OY      235 HLVQALINENPLNG-EVIRLDGA 256
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RESULT 24
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; Sequence 468, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C27
; CURRENT APPLICATION NUMBER: US/09/978, 697

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7	PRIOR FILING DATE: 1997-11-03
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60	PRIOR APPLICATION NUMBER: 60/080328
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75	PRIOR FILING DATE: 1998-04-08

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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

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Matches 86; Conservative 42; Mismatches 114; Indels 21; Gaps 8;

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DB 114 NLGTYLTLKALPYLRKSO-----GNVINTSLVGAIGQAAVYATKATYATMK 166
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QY 235 HLVOAIIENPPLNG-EVIRLDGA 256
DB 227 AAVFLASEANFCGIGIELLVGA 249

RESULT 25

US-09-978-192A-468
Sequence 468, Application US/09978192A

Patent No. US2002017753A1
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Geo, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy Margaret Ann

APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C9
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 22.5% Score 293.5; DB 9; Length 270;
Best Local Similarity 32.7% Fred. No. 1.2e-18;
Matches 86; Conservative 42; Mismatches 114; Indels 21; Gaps 8;

1 MAAARSVKGLVAVITGASGLATAEELVGGASAVLIDLPNSGGEAQRKIGNNVE 60
1 MATGTR-YAKVYVVYVGGRGIGAGYIARFVNSGARVYIDCKDESGRALECEL-PGAYV 58
61 APADVTEKVOYOTALAKRGFRVYVAVACAGIAVASKTYNNKQOTHTLEFQVAVLV 120
59 ILCDVTEDDVKTLVSETIRFRGLDCVYNNAGHPPP-----QREETSAGCFRDLLEL 113
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114 NLCTVTLTLALPYLRKSQ-----GNVINTSLVGAIGQAQAVPYATKGVATMTK 166
181 PIARDLAPIGIRVWTIAPGLFPTLSL-----PEKANTLASQVPPP-SRUDPAEY-A 234
167 ALALDESPYGRVAVICISPGNIMTWPLWELALAMPDPATIREGMLAQPIRGMQPAVEGA 226
235 HLVCATIEENPLNG-EVIRLDGA 256
227 AAVFLASEANFCIGIELLVITGGA 249

Search completed: June 23, 2003, 14:59:49
Job time : 22.333 secs

ALIGNMENTS

RESULT 1

Hypothetical protein F01G4.2 - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000

C:Accession: T20484

R:Haris, B.

submitted to the EMBL Data Library, January 1996

A:Reference number: Z19281

A:Accession: T20484

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-258 <WILD>

A:Cross-references: EMBL:Z68341; PIDN:CAA92764.1; GSPDB:GN00022; CESP:F01G4.2

A:Experimental source: clone F01G4

C:Genetics:

A:Gene: CESP:F01G4.2

A:Map position: 4

A:introns: 8/3; 61/3; 116/3; 162/3; 209/3

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match

57.5%; Score 750; DB 2; Length 258;

Best Local Similarity 59.9%; Pred. No. 8, 1e-51;

Matches 154; Conservative 34; Mismatches 67; Indels 2; Gaps 1;

QY 3 AACRKYGLVAVITGGASGLGATAEKLVGOGASAVLLDLPNSGGEPAAKTKGNVCYAP 62

Db 2 SAURSTKGLVAVITGGASGLGKGAEEVLAAGAQAVALDLPQSGADVAKEIGG--IFTP 59

QY 63 ADTSEKDVQATLALAKGKFRGVDAVNCAGIYAVASKYTNLKKGTHTLEDFQRYLDVNL 122

Db 60 ASTTSEEVRAAFKQAQAGKGLDALVNCAGIYAFKLYSKYKKHVDPEKIRQITDINV 119

QY 123 MGTENVIRLVAGEMGNEPDGGQRCVITNTASVAAFEQGVQAAYASAKGIVGKTLPT 182

Db 120 LGFNIRIRGVALLMGHEKDGANGORCVINTASVAAFQDQOSAYASAKGIVGKTLPT 179

QY 183 ARPLADIGIRVMTIAPGLTSLPEKVNFIASQVFPSPRLGDPAEVAHLVQAIT 242

Db 180 ARFPADGIRFNTIAPGLMDTFLSLPRKVASFLAQLIPNSRLGHPHEYALVQHIT 239

QY 243 NPPLNGEVIRLDGATRM 259

Db 240 MDTNGEITRFDGALRM 256

QY 243 NPPLNGEVIRLDGATRM 259

Db 240 MDTNGEITRFDGALRM 256

QY 243 NPPLNGEVIRLDGATRM 259

Db 240 MDTNGEITRFDGALRM 256

QY 243 NPPLNGEVIRLDGATRM 259

Db 240 MDTNGEITRFDGALRM 256

QY 243 NPPLNGEVIRLDGATRM 259

Db 240 MDTNGEITRFDGALRM 256

QY 243 NPPLNGEVIRLDGATRM 259

Db 240 MDTNGEITRFDGALRM 256

QY 243 NPPLNGEVIRLDGATRM 259

Db 240 MDTNGEITRFDGALRM 256

QY 243 NPPLNGEVIRLDGATRM 259

Db 240 MDTNGEITRFDGALRM 256

QY 243 NPPLNGEVIRLDGATRM 259

Db 240 MDTNGEITRFDGALRM 256

QY 243 NPPLNGEVIRLDGATRM 259

Db 240 MDTNGEITRFDGALRM 256

QY 243 NPPLNGEVIRLDGATRM 259

Db 240 MDTNGEITRFDGALRM 256

QY 243 NPPLNGEVIRLDGATRM 259

Db 240 MDTNGEITRFDGALRM 256

QY 243 NPPLNGEVIRLDGATRM 259

Db 240 MDTNGEITRFDGALRM 256

QY 243 NPPLNGEVIRLDGATRM 259

Db 240 MDTNGEITRFDGALRM 256

QY 243 NPPLNGEVIRLDGATRM 259

Db 240 MDTNGEITRFDGALRM 256

QY 243 NPPLNGEVIRLDGATRM 259

Db 240 MDTNGEITRFDGALRM 256

QY 243 NPPLNGEVIRLDGATRM 259

Db 240 MDTNGEITRFDGALRM 256

QY 243 NPPLNGEVIRLDGATRM 259

Db 240 MDTNGEITRFDGALRM 256

QY 243 NPPLNGEVIRLDGATRM 259

Db 240 MDTNGEITRFDGALRM 256

QY 243 NPPLNGEVIRLDGATRM 259

Db 240 MDTNGEITRFDGALRM 256

QY 243 NPPLNGEVIRLDGATRM 259

Db 240 MDTNGEITRFDGALRM 256

RESULT 3

3-oxoacyl-(acyl-carrier protein) reductase (EC 1.1.1.100) [imported] - *Brucella melit*C:Species: *Brucella melitensis*

C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002

C:Accession: AG3611

R:DelVecchio, V.G.; Kaparat, V.; Redhar, R.J.; Parra, G.; Mujer, C.; Los, T.; Ivanov

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen *Brucella melit*

A:Reference number: AD3252; PMID:11756688

A:Accession: AG3611

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-255 <KUR>

A:Cross-references: GB:AE009916; PIDN:AAU54058.1; PID:q17985013; GSPDB:GN00191

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BMEI10816

A:Map position: II

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

C:Keywords: oxidoreductase

Query Match

54.7%; Score 713; DB 2; Length 255;

Best Local Similarity 57.1%; Pred. No. 5, 9e-48;

Matches 144; Conservative 37; Mismatches 69; Indels 2; Gaps 1;

QY 8 VKGLVAVITGGASGLGATAEKLVGOGASAVLLDLPNSGGEPAAKTKGNVCYAPADYTS 67

Db 3 IENRFLLTGGSSGIGAAVSKMAVEAGAKVLLVNADEAGAKALGASRRFQRTVYAS 62

QY 68 EKDVTATLALAKGKFRGVDAVNCAGIYAVASKYTNLKKGTHTLEDFQRYLDVNLMTFN 127

Db 63 DTDGAAIAAIAEAFSRIDVAVNCAGIYAVASKYTNLKKGTHTLEDFQRYLDVNLMTFN 120

QY 128 VIRLVAGEMGNEPDGGQRCVITNTASVAAFEQGVQAAYASAKGIVGKTLPTIARDLA 187

Db 121 MLRLAAEMAAKNEPDGGQRCVITNTASVAAFEQGVQAAYASAKGIVGKTLPTIARDLA 180

QY 188 PIGIRVMTIAPGLTSLPEKVNFIASQVFPSPRLGDPAEVAHLVQAITENPFLN 247

Db 181 RHGIRVMTIAPGLTSLPEKVNFIASQVFPSPRLGDPAEVAHLVQAITENPFLN 240

QY 248 GEVIRLDGATRM 259

Db 241 GEVIRLDGATRM 252

QY 248 GEVIRLDGATRM 259

Db 241 GEVIRLDGATRM 252

QY 248 GEVIRLDGATRM 259

Db 241 GEVIRLDGATRM 252

QY 248 GEVIRLDGATRM 259

Db 241 GEVIRLDGATRM 252

QY 248 GEVIRLDGATRM 259

Db 241 GEVIRLDGATRM 252

QY 248 GEVIRLDGATRM 259

Db 241 GEVIRLDGATRM 252

QY 248 GEVIRLDGATRM 259

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QY 248 GEVIRLDGATRM 259

Db 241 GEVIRLDGATRM 252

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Db 241 GEVIRLDGATRM 252

QY 248 GEVIRLDGATRM 259

Db 241 GEVIRLDGATRM 252

QY 248 GEVIRLDGATRM 259

Db 241 GEVIRLDGATRM 252

RESULT 4

3-oxoacyl-(acyl-carrier protein) reductase (EC 1.1.1.100) [imported] - *Brucella melit*C:Species: *Brucella melitensis*

C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002

C:Accession: AG3611

R:DelVecchio, V.G.; Kaparat, V.; Redhar, R.J.; Parra, G.; Mujer, C.; Los, T.; Ivanov

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen *Brucella melit*

A:Reference number: AD3252; PMID:11756688

A:Accession: AG3611

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-255 <KUR>

A:Cross-references: GB:AE009916; PIDN:AAU54058.1; PID:q17985013; GSPDB:GN00191

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BMEI10816

A:Map position: II

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

C:Keywords: oxidoreductase

Query Match

54.7%; Score 713; DB 2; Length 255;

Best Local Similarity 57.1%; Pred. No. 5, 9e-48;

Matches 144; Conservative 37; Mismatches 69; Indels 2; Gaps 1;

QY 8 VKGLVAVITGGASGLGATAEKLVGOGASAVLLDLPNSGGEPAAKTKGNVCYAPADYTS 67

Db 3 IENRFLLTGGSSGIGAAVSKMAVEAGAKVLLVNADEAGAKALGASRRFQRTVYAS 62

QY 68 EKDVTATLALAKGKFRGVDAVNCAGIYAVASKYTNLKKGTHTLEDFQRYLDVNLMTFN 127

Db 63 DTDGAAIAAIAEAFSRIDVAVNCAGIYAVASKYTNLKKGTHTLEDFQRYLDVNLMTFN 120

QY 128 VIRLVAGEMGNEPDGGQRCVITNTASVAAFEQGVQAAYASAKGIVGKTLPTIARDLA 187

Db 121 MLRLAAEMAAKNEPDGGQRCVITNTASVAAFEQGVQAAYASAKGIVGKTLPTIARDLA 180

QY 188 PIGIRVMTIAPGLTSLPEKVNFIASQVFPSPRLGDPAEVAHLVQAITENPFLN 247

Db 181 RHGIRVMTIAPGLTSLPEKVNFIASQVFPSPRLGDPAEVAHLVQAITENPFLN 240

QY 248 GEVIRLDGATRM 259

Db 241 GEVIRLDGATRM 252

QY 248 GEVIRLDGATRM 259

Db 241 GEVIRLDGATRM 252

QY 248 GEVIRLDGATRM 259

Db 241 GEVIRLDGATRM 252

QY 248 GEVIRLDGATRM 259

Db 241 GEVIRLDGATRM 252

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Db 241 GEVIRLDGATRM 252

QY 248 GEVIRLDGATRM 259

Db 241 GEVIRLDGATRM 252

QY 248 GEVIRLDGATRM 259

Db 241 GEVIRLDGATRM 252

Thu Jun 26 06:55:04 2003

us-09-931-186-20.rpr

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:23:47 ; Search time 15.6667 Seconds
(without alignments)
1601.559 Million cell updates/sec

Title: US-09-931-186-20
Perfect score: 1304
Sequence: 1 MAACRSYKGLVAVITGAS.....ENPLNGEVRIDGAINMP 261

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_73:*\n1: pir1:*\n2: pir2:*\n3: pir3:*\n4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	750	57.5	258	2	T20484 hypothetical prote
2	722	55.4	255	2	H83326 probable short-cha
3	713	54.7	255	2	AG3611 3-oxoacyl-(acyl)-ca
4	673.5	51.6	250	2	AG7054 probable dehydroge
5	672	51.5	255	2	H95360 probable imported
6	644	49.4	257	2	P97531 probable short-cha
7	644	49.4	257	2	AG2750 3-hydroxyacyl-CoA
8	597	45.8	260	2	C87264 3-hydroxyacyl-CoA
9	382.5	29.3	247	2	E70740 probable fabg2 pro
10	355	27.2	252	2	F83098 probable short-cha
11	345.5	26.5	249	2	F97338 3-ketoacyl-acyl-ca
12	343	26.3	246	2	H72219 3-oxoacyl-(acyl)-ca
13	335.5	25.7	246	2	C83961 3-oxoacyl-(acyl)-ca
14	335.5	25.7	297	2	T51084 3-oxoacyl-(acyl)-ca
15	335	25.7	320	2	S22450 3-oxoacyl-(acyl)-ca
16	334.5	25.7	251	2	AH2042 3-oxoacyl-(acyl)-ca
17	332	25.5	248	2	H84136 3-oxoacyl-(acyl)-ca
18	330.5	25.3	246	2	F82128 3-oxoacyl-(acyl)-ca
19	328.5	25.2	243	2	E97919 3-oxoacyl-(acyl)-ca
20	328.5	25.2	260	2	T36849 probable dehydroge
21	327.5	25.1	243	2	C69508 3-oxoacyl-(acyl)-ca
22	326.5	25.0	243	2	F86721 hypothetical prote
23	317	24.3	249	2	D90481 hypothetical prote
24	316.5	24.3	259	2	H98137 3-oxoacyl-(acyl)-ca
25	316.5	24.3	259	2	AI3149 3-oxoacyl-(acyl)-ca
26	315.5	24.2	260	1	A48154 short-chain alcoh
27	315.5	24.2	296	2	E87260 hypothetical prote
28	313.5	24.0	240	2	H75014 3-oxoacyl-(acyl)-ca
29	313.5	24.0	247	2	S77280 3-oxoacyl-(acyl)-ca
30	313	24.0	247	2	F82776 3-oxoacyl-(acyl)-ca
31	313	24.0	252	2	AB3545 toluenesulfonate z
32	311.5	23.9	244	2	AB0195 3-oxoacyl-(acyl)-ca
33	311.5	23.9	246	2	AB9621 3-oxoacyl-(acyl)-ca
34	310	23.8	256	2	AI0406 probable dehydroge
35	310	23.8	267	2	T11579 probable short cha
36	309	23.7	249	2	AG3121 dehydrogenase Atu4
37	309	23.7	253	2	H98165 3-oxoacyl-(acyl)-ca
38	305.5	23.4	247	2	AG1300 3-ketoacyl-acyl-ca
39	305	23.4	260	2	H70758 probable fabg3 pro
40	303.5	23.3	247	2	AG1672 3-ketoacyl-acyl-ca
41	303	23.2	248	2	H98258 3-oxoacyl-(acyl)-ca
42	303	23.2	248	2	AI3025 3-oxoacyl-(acyl)-ca
43	302	23.2	255	1	S39737 glucose 1-dehydrog
44	302	23.2	255	1	S10707 20beta-hydroxyster
45	300.5	23.0	258	2	C70885 probable dehydroge
46	300.5	23.0	296	2	T26723 hypothetical prote
47	300	23.0	250	1	S47054 probable dehydroge
48	300	23.0	252	2	B90495 hypothetical prote
49	298	22.9	255	2	H84288 3-oxoacyl-(acyl)-ca
50	297	22.8	265	2	T36396 probable short cha
51	296	22.7	245	2	AE3517 3-oxoacyl-(acyl)-ca
52	293.5	22.5	245	2	T12051 3-oxoacyl-(acyl)-ca
53	293	22.5	258	2	D95284 probable imported
54	292.5	22.4	248	2	H70447 3-oxoacyl-(acyl)-ca
55	292	22.4	249	1	B37762 glucose 1-dehydrog
56	292	22.4	272	2	AG3359 3-oxoacyl-(acyl)-ca
57	291.5	22.4	244	1	B42147 short-chain alcoh
58	289.5	22.2	303	2	T46064 3-oxoacyl-(acyl)-ca
59	288.5	22.1	244	2	C90812 3-oxoacyl-(acyl)-ca
60	288.5	22.1	244	2	C85672 3-oxoacyl-(acyl)-ca
61	288	22.1	263	2	AB0812 probable oxidoredu
62	287.5	22.0	246	1	RDALAE acetateacyl-CoA re
63	287.5	22.0	254	1	G75313 3-oxoacyl-acyl car
64	285.5	21.9	244	2	AD0642 3-oxoacyl-(acyl)-ca
65	285.5	21.9	257	1	A72395 oxidoreductase, sh
66	285	21.9	255	2	C82644 2,5-dichloro-2,5-c
67	284.5	21.8	253	1	B86737 acetyl dehydrogen
68	284.5	21.8	256	2	E72427 oxidoreductase, sh
69	284.5	21.8	272	2	A99950 hypothetical prote
70	283.5	21.7	246	1	DEKCMG acetateacyl-CoA re
71	283	21.7	258	2	B89773 acetoindiacetyl)r
72	282.5	21.7	521	2	C87474 hypothetical prote
73	281.5	21.6	248	2	E81695 3-oxoacyl-(acyl)-ca
74	281	21.5	255	2	D72377 oxidoreductase, sh
75	279.5	21.4	260	2	F82954 probable short-cha
76	279.5	21.4	241	1	S06998 acetateacyl-CoA re
77	279	21.4	240	2	F87312 acetateacyl-CoA re
78	279	21.4	262	2	B97588 oxidoreductase, sh
79	279	21.4	262	2	AG2809 short chain dehydr
80	278.5	21.4	289	2	D69835 glucose 1-dehydrog
81	277	21.2	246	1	E99279 acetateacyl-CoA re
82	276.5	21.2	248	2	B57223 probable 3-ketoacy
83	276.5	21.2	286	2	G63378 probable short-cha
84	276	21.2	249	1	A11841 bile acid dehydrox
85	276	21.2	259	2	E95903 probable dehydroge
86	276	21.2	263	2	S01237 glucose 1-dehydrog
87	276	21.2	267	2	B87578 hypothetical prote
88	276	21.2	285	1	A65017 probable 3-oxoacyl
89	276	21.2	285	2	A11041 probable oxidoredu
90	276	21.2	285	2	D85885 probable oxidoredu
91	275.5	21.1	248	2	T44361 acetateacyl-CoA re
92	275	21.1	319	2	S22416 3-oxoacyl-(acyl)-ca
93	274.5	21.1	244	2	T44434 3-oxoacyl-(acyl)-ca
94	272.5	20.9	240	2	S75021 3-ketoacyl-acyl-ca
95	272.5	20.9	241	2	AI2916 acetateacyl-CoA re
96	272.5	20.9	245	2	D97691 acetateacyl-CoA re
97	272.5	20.9	248	2	F71538 probable 3-oxoacyl
98	272.5	20.9	262	2	S02299 glucose 1-dehydrog
99	272	20.9	251	2	G72389 oxidoreductase, sh
100	271.5	20.8	246	2	B89896 3-oxoacyl-(acyl)-ca

DT 01-OCT-1994 (Rel. 30, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Oxidoreductase ucpa (EC 1.1.1.36).
 DE ucpa OR STM245 OR STY2682.
 OS Salmonella typhimurium, and
 OS Salmonella typh.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 NC NCBI_TaxID=602, 601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.typhimurium; STRAIN=LT2 / SSGC1412 / ATCC 700720;
 RX MEDLINE=21534946; PubMed=11677609;
 RA McCelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Potwilk S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan H., Flores L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 RT LT2."
 RL Nature 413:852-856(2001).
 RN [2]
 RP SEQUENCE OF 204-263 FROM N.A.
 RC SPECIES=S.typhimurium;
 RX MEDLINE=91358382; PubMed=1909324;
 RA Hyattley M.M., Kredich N.M.;
 RT "The cysP promoter of Salmonella typhimurium: characterization of two
 RT binding sites for CysB protein, studies of in vivo transcription
 RT initiation, and demonstration of the anti-inducer effects of
 RT thiosulfate."
 RL J. Bacteriol. 173:5876-5886(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.typh; STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parshall J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Seakins M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Croft A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Felwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagsels K.,
 RA Krohn A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrett B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typh CT18."
 RL Nature 413:848-852(2001).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
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 CC
 CC EMBL, AE008810; AAL21339.1; -
 CC EMBL, AL627274; CAD07676.1; -
 CC PIR, A38121; A38121.
 DR StGene: SG10424; ucpa.
 DR InterPro: IPR002198; ADH_short.
 DR PROSITE: PS00061; ADH_SHORT; FALSE_NG.
 KW Oxidoreductase; Complete proteome.
 FT CONFLICT 218 L -> M (IN REF. 2).
 FT CONFLICT 258 S -> T (IN REF. 2).
 FT CONFLICT 263 V -> I (IN REF. 2).
 SO SEQUENCE 263 AA; 27870 MW; 81B26CADD94D534E CRC64;

QY 10 GIVAVITGAGSLGLATATRELVGOCASAVLDDLPNSGGEAOAKL-----GNNCFAP 62
 Db 6 GTALITGASGIGIGIARVFARHGANILDISD-----ELEKLADELGRGRCTAVK 60
 QY 63 ADVTSEKDYGTALALAKGKFGADVAVACAGIAVASKTYNLKKGQTHLEDFORPLDYNL 122
 Db 61 ADVRFASVQAQAAVAAKKEGKIDILVNNAGVCGRGNLDNSE-----EDRDFIDINI 114
 QY 123 MGTFTVIRLVAGEMQONEPDGOGVLIINFASVA-TEGQVQAAYASKSGIVGKFLP 181
 Db 115 KGVNVTKAVLPEMIKRD-----GRIVMSSVGVMDVADGETAVYALSKRAIVGLTRK 168
 QY 182 IARDLAPIGIRMTIAPGLFGPRLTST-----PEKVFNLASOVFPFRLGDPAY 233
 Db 169 LAVERAQSIRVNAICPGIVRTIPMAESIRQSNPDPEVLTAKAIPL-RLADPLV 227
 QY 234 ARLVQ--ATLENPLNGEVIRLDG 255
 Db 228 GELAAFLADESSYLGTQNVIDG 251

RESULT 23
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 ID PHBB_ALCEU STANDARD; PRT; 246 AA.
 AC P14697;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acetoacetyl-CoA reductase (EC 1.1.1.36).
 GN PHBB.
 OS Alcaligenes eutrophus (Ralstonia eutropha).
 OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
 OC Ralstonia.
 OC NCBI_TaxID=510;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H16 / DSM 428 / ATCC 17689;
 RX MEDLINE=8935356; PubMed=2670935;
 RA Peoples O.P., Sinskey A.J.;
 RT "Poly-beta-hydroxybutyrate biosynthesis in Alcaligenes eutrophus H16.
 RT Characterization of the genes encoding beta-ketothiolase and
 RT acetoacetyl-CoA reductase."
 RL J. Biol. Chem. 264:15293-15297(1989).
 CC -1- CATALYTIC ACTIVITY: (R)-3-hydroxyacyl-CoA + NADP(+) = 3-oxoacyl-
 CC CoA + NADPH.
 CC -1- PATHWAY: Poly-beta-hydroxybutyrate biosynthesis; second step.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
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 CC EMBL, J04987; AAA21973.1; -
 CC PIR, B34340; RDAIAE.
 DR HSSP: O70351; IE3S.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Oxidoreductase; NADP; PHB biosynthesis.
 FT NP_BIND 8 NADP (BY SIMILARITY).
 FT ACT_SITE 32 BY SIMILARITY.
 SO SEQUENCE 246 AA; 26370 MW; AD6739E0F5C93C06 CRC64;

EMBL; M15813; AAB61153.1; -
 DR PIR: A28212; A28212.
 DR PIR: A26938; A26938.
 DR PIR: B37762; B37762.
 DR HSSP; P19992; 1HDC.
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF0106; adh_short; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 DR Oxidoreductase; NAD, Bile acid catabolism; Multigene family.
 FT NP_BIND 7 13
 FT NP_BIND 32 36 NAD (POTENTIAL).
 FT ACT_SITE 157 157 BY SIMILARITY.
 FT CONFLICT 159 162 TSRA -> YGGG (IN REF. 2).
 SQ SEQUENCE 249 AA; 26658 MW; 084E380921D72C93 CRC64;

Query Match 22.4%; Score 292; DB 1; Length 249;
 Best Local Similarity 30.7%; Pred. No. 1.5e-15;
 Matches 83; Conservative 45; Mismatches 98; Indels 44; Gaps 10;

OY 8 VKGLVAVITGGASGIGLATAERLYGQASAVLLDLPNSGE-----AQAKK----- 53
 DB 4 VQDKRTITGGTRGIGFAAKLFENGAKVSIF-----GETQEVDPALAKELYPEE 57
 OY 54 -LGNNGVFAPADVTSEKDVOTALALAKGFRVDVAVNCAGIVASKTYMLKGGQHTL 111
 DB 58 EVLG----FAP-DLTSRDVAAVGTVAQKGRGLDVMNNAGITMNGVFSVSE----- 106
 OY 112 EDFQRYLDVNLMTFTVIRLVAGEKQNEPDQSGRGVITFASVAAFEQGVGAAYSAS 171
 DB 107 EDFKIMDINWGVFN-----GMSAVQCKMKDKOGVITNTASTGTIGSLGIGYPTS 160
 OY 172 KGGIVGMLPTARADAPLIGIRVMTAPGLFTPLTSLPEVAVNFASQVFPRLDDPA 231
 DB 161 KAGVIGLTHGLREIRKININVGAFAPVVDIMTKGLPRLIDYLKTLPM-KRMKPE 219
 OY 232 EYALHVAIENPFNG---EYIRIDGAIR 258
 DB 220 EIAN-VYFLASDLASGITATTISVDGAYR 248

RESULT 21
 FARG_ECOLI STANDARD; PRT: 244 AA.

AC F25716; P789221;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 3-oxoacyl-acyl-carrier protein reductase (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase).
 GN FARG OR B1093.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_Taxid=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Rawlings M., Cronan J.E. Jr.;
 RT "The gene encoding Escherichia coli acyl carrier protein lies within a cluster of fatty acid biosynthetic genes.";
 RL J Biol. Chem. 267:5751-5754(1992).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Colado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";

RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE=97061202; PubMed=8905232;
 RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horinouchi T.;
 RA "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
 RT DNA Res. 3:137-155(1996).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] + NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
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EMBL; M84991; AAA23739.1; -
 DR EMBL; AE000210; AAC74177.1; -
 DR EMBL; D90745; BAA35901.1; -
 DR PIR; B42147; B42147.
 DR HSSP; P29132; 1DEF.
 DR Ecogene; EGI1318; fabg.
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 DE Fatty acid biosynthesis; Oxidoreductase; NADP, Complete proteome.
 GN NP_BIND 10 34
 GN ACT_SITE 151 151 NADP (BY SIMILARITY).
 GN CONFLICT 30 30 BY SIMILARITY.
 FT A -> G (IN REF. 1).
 SQ SEQUENCE 244 AA; 25560 MW; 48C1F2A7FEEDD9 CRC64;

Query Match 22.4%; Score 291.5; DB 1; Length 244;
 Best Local Similarity 30.0%; Pred. No. 1.6e-15;
 Matches 76; Conservative 50; Mismatches 112; Indels 15; Gaps 4;

OY 9 KGLVAVITGGASGIGLATAERLYGQASAVLLDLPNSGEPQAKKLGNNCFAPADVTSE 68
 DB 4 EGRALVTGASRGGRALAFETLAARGAKVIGTATSENGAQAISDYCGANGKGLMVTDP 63
 OY 69 KDVOITALALAKGFRVDVAVNCAGIVASKTYMLKGGQHTLEDDQRYLDVNLMTFTV 128
 DB 64 ASIESVLEKTRAERGEVDILVNNAGITRDMILRMKD-----EENWDITNLSVERK 117
 OY 129 IRLVAGEKQNEPDQSGRGVITFASVAAFEQGVGAAYSASAGKIGVGTLPILARDLP 188
 DB 118 SKAVMRAMMK-----RHGRITIGSVVTMNGGAGNAAKAGLIGSKSLAEVAS 171
 OY 189 IGRVMTIADGLEGTPLTSLPEKAVNFASQVFPRLDDPAEYALVO--AIENPPL 246
 DB 172 RGIIVNVVAPGFETDTRALSDQFAGILAYVP-AGRLGAQEIANAFAFLASDEAYI 230
 OY 247 NGEVIRLDGAIRM 259
 DB 231 TGETLHVNGGMYM 243

RESULT 22
 UCPA_SALTY STANDARD; PRT: 263 AA.
 ID UCPA_SALTY
 AC B37471

DB 116 RMSAAVIRGMMKK-----RAGRIIVGSGVYGTNGNAGOTNYAAAKAGVIGFTKSAREV 169
QY 187 APIGIRVMTIAPGLFGTPLLTSLEPKVANFLASQVPPSRIGDPAEVAHLV--QATLENP 244
DB 170 ASRGVTVNTVAPGFIETDMTKALNDQRAATLISNV-AGRIQDERIETASAVFLASPEAA 228
QY 245 FLNGEYIRLDGAIKM 259
DB 229 YITGETLHVNGMYM 243

RESULT 19

FABG_AQUAE STANDARD: PRT: 248 AA.

ID FABG_AQUAE STANDARD: PRT: 248 AA.
AC 06/610;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase).
GN FABG OR NO.1716.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
OC Aquifex.
OX NCBI_Taxid=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RA MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Grahman D.E., Overbeek R., Sneed M.A., Keller M., AuJay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.,
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus".
RT Nature 392:353-358(1998).
RL Nature 392:353-358(1998).
CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
CC NAD(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
CC PATHWAY.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDOCTASES
CC (SDR) FAMILY.
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL: AE000752; AAC07575.1; -
DR HSSP: P50163; ZAE1.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT.1.
KM Fatty acid biosynthesis; Oxidoreductase; NADP: Complete proteome.
FT NP_BIND 12 36 NADP (BY SIMILARITY).
FT ACT_SITE 157 157 BY SIMILARITY.
SQ SEQUENCE 248 AA; 26867 MW; 5CED9EB9AD83FE2C5 CRC64;

Query Match 22.4%; Score 292.5; DB 1; Length 248;
Best local similarity 30.0%; Pred. No. 1.4e-15;
Matches 77; Conservative 50; Mismatches 109; Indels 21; Gaps 6;

QY 8 VKLVAVITGGASGLATRAERLVGGASAVLLDLPNSGGEQAOKLGN-----NCFARA 63
DB 5 LQKRVSLVYGSTGIGRAIAEKLAGAGSVYITGTSCEAKAVAEIANKYGVKAHGVEM 64
QY 64 DVSEKDVGCTALALAGKFGKRVAVNVCAGIAVAASKTYMLKKGQETLEDFOFVLDVNLK 123

QY 124 GFENVIRLVAGEMGQNEPDGGOR-GVITNTASVAFAEGVGOAAYSAKSGIVGKTLPI 182
DB 119 GFELVYQNSLRKMK-----QRMCRIVNISSVGFITNCQVNISTRKALIGFTKSL 171
QY 183 ARDLAPIGIRVMTIAPGLFGTPLLTSLEPKVANFLASQVPPSRIGDPAEVAHLVQALTE 242
DB 172 AKELAPRVNLVNVAVAPGFIETDMTAVLSEIKQKYEQIPL-GRGSPREAVANVYLQCS 230
QY 243 N--PFLNGEYIRLDGAI 257
DB 231 ELASVITGEYIVHNGM 247

RESULT 20

BA71_EUBSP STANDARD: PRT: 249 AA.

ID BA71_EUBSP STANDARD: PRT: 249 AA.
AC P07914;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 7-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.159) (Bile acid 7-dehydroxylase) (7-alpha-HSDH) (Bile acid-inducible protein).
GN BA71 AND BA1A3.
OS Eubacterium sp. (strain VPI 12708).
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_Taxid=29347;
RN [1]
RP SEQUENCE FROM N.A. (BA1A3).
RA MEDLINE=90330548; PubMed=2376563;
RA Gopal-Srivastava R., Mallonee D.H., White W.B., Hylemon P.B.,
RA "Multiple copies of a bile acid-inducible gene in Eubacterium sp.
RT strain VPI 12708.";
RT J. Bacteriol. 172:4420-4426(1990).
RL J. Bacteriol. 172:4420-4426(1990).
RN [2]
RP SEQUENCE FROM N.A. (BA1A1).
RA MEDLINE=88197993; PubMed=2834320;
RA Coleman J.P., White W.B., Lijewski M., Hylemon P.B.,
RA "Nucleotide sequence and regulation of a gene involved in bile acid
RT 7-dehydroxylation by Eubacterium sp. strain VPI 12708.";
RT J. Bacteriol. 170:2070-2077(1988).
RL J. Bacteriol. 170:2070-2077(1988).
RN [3]
RP SEQUENCE OF 1-55 FROM N.A. (BA1A1), AND SEQUENCE OF 1-33.
RA MEDLINE=87165759; PubMed=3549693;
RA Coleman J.P., White W.B., Hylemon P.B.,
RA "Molecular cloning of bile acid 7-dehydroxylase from Eubacterium sp.
RT strain VPI 12708.";
RT J. Bacteriol. 169:1516-1521(1987).
RL J. Bacteriol. 169:1516-1521(1987).
CC -1- FUNCTION: 7-ALPHA-DEHYDROXYLATION OF CHOLIC ACID, YIELDING
CC DEOXYCHOLIC ACID AND LITHOCHOLIC ACID, RESPECTIVELY. HIGHEST
CC AFFINITY WITH TAUROCHENODEOXYCHOLIC ACID.
CC -1- CATALYTIC ACTIVITY: 3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-
CC cholanate + NAD(+) = 3-alpha,12-alpha-dihydroxy-7-oxo-5-beta-
CC cholanate + NADH.
CC -1- PATHWAY: Bile acid catabolism.
CC -1- INDUCTION: PRESENCE OF C(24) BILE ACIDS CONTAINING A
CC 7-ALPHA-HYDROXY GROUP.
CC -1- SIMILARITY: THERE ARE THREE GENES FOR BILE ACID PROTEINS: BA1A1 IS
CC IDENTICAL TO BA1A3 AND THERE IS 81% IDENTITY WITH BA1A2.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDOCTASES
CC (SDR) FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch).
CC EMBL: M34658; AAB61155.1; -

QY 239 AITE--NPELNGEYRLDGAIRMQ 260
 Db 232 FLASDLSSYMTGSALTADGGYTAQ 255

RESULT 17

YAVI_RHISN STANDARD; PRT; 548 AA.
 ID YAVI_RHISN
 AC 053217;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Putative short-chain type dehydrogenase/reductase YAVI (EC 1.1.1.100).
 GN YAVI.
 OS Rhizobium sp. (strain NGR234).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=394;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97305956; PubMed=9163424;
 RA Freberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
 RT "Molecular basis of symbiosis between Rhizobium and legumes."
 RL Nature 387:394-401(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96389014; PubMed=8796346;
 RA Freberg C., Perret X., Broughton W.J., Rosenthal A.,
 RT "Sequencing the 500-kb GC-rich symbiotic region of Rhizobium sp.
 NGR234 using dye terminators and a thermostable 'sequenase': a
 beginning."
 RL Genome Res. 6:590-600(1996).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 (SDR) FAMILY. CONTAINS TWO DOMAINS.
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 or send an email to license@isb-sib.ch).
 CC EMBL: Z68203; CAA92424.1; AL1-INIT.
 DR EMBL: AEO00101; AAB91897.1;
 DR HSSP: P50163; ZAE1
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 2.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
 KM Multifunctional enzyme.
 FT DOMAIN 1 250
 FT DOMAIN 2 271
 FT NP_BIND 12 548
 FT NP_BIND 37 548
 FT ACT_SITE 154 154
 FT NP_BIND 280 304
 FT ACT_SITE 420 420
 FT ACT_SITE 420 420
 SQ SEQUENCE 548 AA; 57593 MW; 399598C5DF17C23F CRC64;

Query Match 22.74; Score 296.5; DB 1; Length 548;
 Best Local Similarity 33.68; Pred. No. 1.7e-15;
 Matches 86; Conservative 40; Mismatches 101; Indels 29; Gaps 8;

QY 10 GLVAVITGGASGLATATERTLVGOGASAVLLDLPNSGGEAQAQKLGNNCVFAPADYTSK 69
 Db 9 GRVAVITGGASGLATATERTLVGOGASAVLLDLPNSGGEAQAQKLGNNCVFAPADYTSK 68
 QY 70 DVCATATLAKGKGRVDVAVNCAGI-----AVASKTYNKKGGTHLEDFORVLDVNLGTF 125
 Db 69 DVVALRLLEKRRSRLEVLVNNAGIGPTMAATADT-----ALEDFORVLDVNLGTF 119

QY 126 FNVIKLVAGEMGQNEPDGQGRGVITINTASVAFAEGOVGGAASAKGCIWETLPARD 185
 Db 120 YSVACETIAKLM-----KRG-----AAIVNVAFLADLGNPKRSNAAKAGLITSTKSLAOR 171
 QY 186 LAPGIRVMTIAPGLFGTLPILTSLPERVANE-----LASQVPPSPRLGDPATVIAHLVQ--A 239
 Db 172 WASRGIRVAVAGCHVTPVAVAEI-ERACKLDVSAIRRRVPL-GRVAPDEIAFAVAFELA 229
 QY 240 ILENPFLNGEYRLDQ 255
 Db 230 SAQASITTGSTLYVDG 245

RESULT 18

FABG_VIBHA STANDARD; PRT; 244 AA.
 ID FABG_VIBHA
 AC P55336;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
 acyl carrier protein reductase).
 GN FABG.
 OS Vibrio parvulus.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=669;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B392;
 RX MEDLINE=96134997; PubMed=8550484;
 RA Shen Z., Byers D.M.;
 RT "Isolation of Vibrio parvulus acyl carrier protein and the fabg, acpp,
 and fabf genes involved in fatty acid biosynthesis."
 RL J. Bacteriol. 178:571-573(1996).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 (SDR) FAMILY.
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 or send an email to license@isb-sib.ch).
 CC EMBL: U39441; AAC43589.1;
 DR HSSP: P19992; IHDC.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Fatty acid biosynthesis; Oxidoreductase; NADP.
 FT NP_BIND 10 34
 FT NP_BIND 131 151
 FT ACT_SITE 151 151
 SQ SEQUENCE 244 AA; 25519 MW; FC41A1C65B8CDAAA CRC64;

Query Match 22.5%; Score 293.5; DB 1; Length 244;
 Best Local Similarity 29.8%; Pred. No. 1.1e-15;
 Matches 76; Conservative 51; Mismatches 113; Indels 15; Gaps 4;

QY 7 SVKGLVAVITGGASGLATATERTLVGOGASAVLLDLPNSGGEAQAQKLGNNCVFAPADY 66
 Db 2 NLEGRVAVITGGASGLATATERTLVGOGASAVLLDLPNSGGEAQAQKLGNNCVFAPADY 61
 QY 67 SEKDVQATLALAKGKGRVDVAVNCAGI-----AVASKTYNKKGGTHLEDFORVLDVNLGTF 126
 Db 62 DVESEIATLTKINDECGAIDLIVNNAAGITRNLMLRKD-----DEMNDIINTNLPIY 115
 QY 127 NVIRLVAGEMGQNEPDGQGRGVITINTASVAFAEGOVGGAASAKGCIWETLPARD 186

Proc. Natl. Acad. Sci. U.S.A. 88:10064-10068(1991).
 -1- CATALYTIC ACTIVITY: Androstane-3-alpha,17-beta-diol + NAD(+) = 17-beta-hydroxyandrostane-3-one + NADH.
 -1- SUBUNIT: HOMOTETRAMER.
 -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
 PIR: S10707; S10707.
 DR: 2HSD; 31 AUG-94.
 DR: PDB: 1HDC; 07-FEB-95.
 DR: InterPro: IPR002198; ADH_short.
 DR: Pfam: PF00106; adh_short; 1.
 DR: PRINTS: PR00080; SDRFAMILY.
 DR: PROSITE: PS00061; ADH_SHORT; 1.
 KM: Oxidoreductase; NAD: Steroid metabolism; 3D-structure.
 FT: NP_BIND 10 34 NAD (BY SIMILARITY).
 FT: ACT_SITE 152 152
 SQ: SEQUENCE 255 AA; 26484 MW; 9CB93CB66A628D5 CRC64;
 Query Match 23.2%; Score 302; DB 1; Length 255;
 Best Local Similarity 33.6%; Pred. No. 2.7e-16;
 Matches 85; Conservative 47; Mismatches 101; Indels 20; Gaps 8;
 QY 8 VKGLAVITGASGLGATPARELVGOGASAVLLDIPNSGDAQAKIGNCVPADYTS 67
 DB 4 LSGKTVITGARGIGAEARQAQAVAGARVVLADVLEDEGAATARELDAAKYOHLDVTI 63
 QY 68 EEDVGTALAKGKRGVDVAVNCAGIYASVSKTYLKKGGHTLEDFQVLDVNLGTFEN 127
 DB 64 EEDMORVAVYAREEGSYDGLVNNAGISTGMFL-----EHSVRFKRYVDINLTGVTI 117
 QY 128 VTRLVAGEQNEPDGQGRVYINTASVAAFEQGVGAQVSAKSGIVGMLPIARDLA 187
 DB 118 GKRTYIPAV---KDAGC--GSIVISSAGLGMALTSYSGASKWGVGSKLAAYELG 171
 QY 188 PGIRMTAPGLFGTPLL--TSLPEKAVNFIASQVPPSRUG-DPAEYAHVQAIRP-- 242
 DB 172 TPRIRVNSVHPGMYTTPMARETGINQSGNT--PTPM-GRVGNPGELIAGVYVLLSDT 228
 QY 243 NPLNGEVIRLDG 255
 DB 229 SSYVTGAELAVDG 241
 RESULT 16
 YWFD_BACSU STANDARD; PRT; 255 AA.
 ID YWFD_BACSU STANDARD; PRT; 255 AA.
 AC P39640;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical oxidoreductase ywfd (EC 1.-.-.-).
 GN YWFD OR IPA-82D.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_Taxid=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=95020537; PubMed=7934828;
 RA Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,
 RA Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Mosser I.,
 RA Presacat E., Santana M., Schneider E., Schweizer J., Vertes A.,
 RA Rapoport G., Danchin A.;
 RT "Bacillus subtilis genome project: cloning and sequencing of the 97 kb region from 325 degrees to 333 degrees";
 RL MOL. Microbiol. 10:371-384(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Aarevedo V., Bertorello M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.U., Cornerton I.F., Cummings N.J., Daniel R.A.,
 RA Denicot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Ertan K.D., Errington J., Fabre C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Funa S., Gallizi A., Galleron N.,
 RA Gilm S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
 RA Gutseppe G., Guy B.J., Haga K., Haeck J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koelter P., Konigstein G., Krogh S., Kunnano M.,
 RA Kurita K., Lapides A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Potwollik S., Prescott A.M.,
 RA Prescecian E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale I.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scofield F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Solio B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vanier F., Vassarotti A.,
 RA Viart A., Wandut R., Wedler E., Wedler H., Weitenegger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis";
 RL Nature 390:249-256(1997).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
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 CC
 CC EMBL: X73124; CA51638.1; -;
 CC EMBL: Z99123; CAB1579.1; -;
 CC PIR: S39737; S39737.
 CC HSSP: P50162; IAE1.
 CC Subtilist; BG10628; ywfd.
 CC InterPro: IPR002198; ADH_short.
 CC Pfam: PF00106; adh_short; 1.
 CC PRINTS: PR00080; SDRFAMILY.
 CC PROSITE: PS00061; ADH_SHORT; 1.
 CC Hypothetical protein; Oxidoreductase; Complete proteome.
 FT NP_BIND 11 33 NAD OR NADP (BY SIMILARITY).
 FT ACT_SITE 154 154 BY SIMILARITY.
 SQ SEQUENCE 255 AA; 27324 MW; 20AA2259F8B8C9B CRC64;
 Query Match 23.2%; Score 302; DB 1; Length 255;
 Best Local Similarity 32.6%; Pred. No. 2.7e-16;
 Matches 86; Conservative 41; Mismatches 101; Indels 36; Gaps 7;
 QY 14 VITGASGLGATPARELVGOGASAVLLDIPNSGDAQAKIGNCV-FAPADYTSKDVQ 72
 DB 11 LITGASGIGYAAVQAFAGQAAVYVADIDAGQEAAMRKNNDRHFVOTDITDEACQ 70
 QY 73 TALALAKGKRGVDVAVNCAGIYASVSKTYLKKGGHTLEDFQVLDVNLGTFENVR-- 130
 DB 71 HAVESAVTFEGGLDVLINNAGIEIVAPHEHE-----LSDVMNVLYVNLGFMISKHA 124
 QY 131 ----LVAGEMQNEPDGQGRVYINTASVAAFEQGVGAQVSAKSGIVGMLPIARDL 186
 DB 125 LKHLIAG-----KGNIIINCSVGLVAMPDIPAYNASKGVGLDITSMADV 172
 QY 187 APGIRVMTAPGLFGTPLL-----LTSLEKAVNFIASQVPPSRUGDPADYAHVQ 238
 DB 173 AKHQIRVNCVOPGIDTFLNKSFLNNEGTLIEIKREKAKVNDL-LRLGPEIRIAYML 231

NP_BIND 9 33 NADP (BY SIMILARITY).
 FT ACT_SITE 154 154 BY SIMILARITY.
 FT CONFLICT 23 23 D -> A (IN REF. 1).
 SQ SEQUENCE 246 AA; 26282 MM; C6A391167D237DC CRC64;
 Query Match 23.9%; Score 311.5; DB 1; Length 246;
 Best Local Similarity 29.7%; Pred. No. 4.8e-17;
 Matches 76; Conservative 55; Mismatches 100; Indels 25; Gaps 6;

13 AVITGGAGGCGTAAETLVGQASAVLLDLPNSGGECA-----KKGNNCVFAPADY 65
 7 AIVGAGRGIGRSTALDLAKSGANV---VNSGENEKAEEVDEIKSMGRKAIKADY 63
 66 TSEKDVOTATLALAKGKRGVDVAVNCAGIYASRTYLNKRGQHTLEDFQRLVDVNLMT 125
 64 SNPEDVQNMKEITLSTVSTIDILVNNAGITRDNLIMMKE-----DEMDDVINILKGV 117
 126 FNVIRLYAGEMGQNEPDGQGRGVIINTASVAAFEGVGGAASASKGIYGTLPITARD 185
 118 FNCRTAVTRQMKR-----RSGRIIVSSIVGVSGNPGQANYAAAGAYIGLTKSSAKE 171
 186 LAPGIRVMTAPGLFTPLTSLPERKAVNFASQVFPSPRLGDPAAVHLYOATLEN-- 243
 172 LASNITVYNAIAPFISTDMTDKIAKVDQEMLKQITL-ARFGPSDVSSVTFLESGA 230
 244 PFLNGEVIRLDGATRM 259
 231 RYMTGQTLHIDGMVM 246

RESULT 14
 YK02_MYCTU STANDARD; PRT; 260 AA.
 ID YK02_MYCTU
 AC Q10855;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Putative oxidoreductase Rv2002 (EC 1.-.-.-).
 GN FABG3 OR Rv2002 OR MT2058 OR MTCY39.16C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RC MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Petwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
 RA "Deciphering the Biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."
 RL Nature 393:537-544(1998).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Milada A.,
 RA Bishai W.;
 RA "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains."
 RL Submitted (APR-2001) to the EMBL/Genbank/DBD databases.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: 274025; CAA98414.1;
 DR EMBL: AE007057; AAK46335.1;
 DR HSSP: P19992; LHDC.
 DR TIGR: MT2058;
 DR TubercuList: Rv2002;
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
 FT NP_BIND 11 35
 FT ACT_SITE 153 153
 FT CONFLICT 174 174 S -> G (IN REF. 2).
 SQ SEQUENCE 260 AA; 27030 MM; 0935A14ED36220B7 CRC64;
 Query Match 23.4%; Score 305; DB 1; Length 260;
 Best Local Similarity 33.9%; Pred. No. 1.6e-16;
 Matches 85; Conservative 41; Mismatches 99; Indels 26; Gaps 5;

10 GCVAVITGGAGGCGTAAETLVGQASAVLLDLPNSGGECAKKGNNCVFAPADVTSBK 69
 7 GKVALVSGARGGASHVPAWNAEAKVFGDILDEGRVAAEADAAARIYHLDVTPA 66
 70 DVQATALAKGKRGVDVAVNCAGIYASRTYLNKRGQHTLEDFQRLVDVNLMTGFNY 129
 67 QWTAADVDTAVTAPAGLHVLNNAGI-----INIGTIEDYALTEMRILDVNLTVGLGI 120
 130 RLYVAGEMGQNEPDGQGRGVIINTASVAAFEGVGGAASASKGIYGTLPITARDLAPI 189
 121 RAVV-----KPKKEKRGSIINISIEGLAGTVACHGTYTAFRAVGLTKSTALELPS 174
 190 GIRVMTAPGLFTPLTSLPERKAVNFASQVFPSPRLG---DPAVHLY--QAIIENP 244
 175 GIIVNSIHPELVTPMTDWPEDI-----FQALGRAAPEVSVMLVYVLADESS 225
 245 FLNGEVIRLDG 255
 226 YSTGAERFVDG 236

RESULT 15
 2BHD_STREX STANDARD; PRT; 255 AA.
 ID 2BHD_STREX
 AC P19992;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE 20 beta-hydroxysteroid dehydrogenase (EC 1.1.1.53).
 DE Streptomyces exfoliatus (Streptomyces hydrogeneus).
 OS Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1905;
 [1]
 RP SEQUENCE.
 RC MEDLINE=90306362; PubMed=2194840;
 RA Marekov L., Krock M., Joernvall H.;
 RA "Prokaryotic 20 beta-hydroxysteroid dehydrogenase is an enzyme of the
 RT 'short-chain non-metalloenzyme' alcohol dehydrogenase type-";
 RL FEMS Lett. 266:51-54(1990).
 [2]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RC MEDLINE=92052211; PubMed=1946424;
 RA Ghosh D., Weeks C.M., Grochulski P., Duax W.L., Erman M.,
 RA Rimsay R.L., Orr J.C.;
 RA "Three-dimensional structure of holo 3 alpha,20 beta-hydroxysteroid
 RT dehydrogenase: a member of a short-chain dehydrogenase family.";

CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NAD(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SCD) FAMILY.
 CC -----
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 CC or send an email to license@sdb-sdb.ch).

CC EMBL: D90907; BAA17614.1; -
 DR HSSP: P50162; 1AET.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PRO0080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR Fatty acid biosynthesis; Oxidoreductase; NADP: Complete proteome.
 FT NE_BIND 11 35
 FT ACT_SITE 156 156 NADP (BY SIMILARITY).
 FT SEQUENCE 247 AA; 25724 MW; 91EBF9409C77F20 CRC64;
 SQ

Query Match 24.0%; Score 313.5; DB 1; Length 247;
 Best Local Similarity 32.1%; Pred. MisMatches 92; Indels 43; Gaps 8;
 Matches 85; Conservativity 45;

QY 12 VAVITGGASGLGATLERLYGQ-----ASAYLDLPSSGGEAAKRGNNC 58
 DQ 8 VALVTGASRGIGKATLALATMKVYVNAOSSTADAVAEITLNGEA----- 58
 QY 59 VFAPADVTSKEDVQTALALAKFKGVDYAVNCAJIAVASKYTNLKGGTHLEDFQRYL 118
 DQ 59 IAVQANVANDVDQILKTLDFSRDYLNNAGITRDLILRMK-----LEDNQAVI 112
 QY 119 DVNLMTGFNTRILVAGMGQNEPDQGGQRCVITNTSVAFEEQVQGAAYSASAKGIVGN 178
 DQ 113 DLNLTGYFLCTKAVSKMLKQ-----KSGRIINISVAGMKNPQANISAKKAGVIFR 166
 QY 179 TLPIARDLAPIGIRVMTIAPGLFGTPLLTSL-PEKVANFLASQVPPSRUGDPAEYAHLY 237
 DQ 167 TKYVAKELASRGYVNAVNAFCFATLMDTEENLNEPILOF-----IPL-ARYGQPEYVAGTI 221
 QY 238 QAITENP---FLNGEVIRLDGAIRM 259
 DQ 222 RFLATDPAALVITGQTFNVGVGMW 246

RESULT 13
 FABG_BACSU STANDARD: PRT; 246 AA.
 ID FABG_BACSU
 AC P51831; O311733;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
 DE acyl carrier protein reductase).
 GN FABG.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 CX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=96326321; PubMed=8759840;
 RA Morbidoni H.R., de Mendoza D., Cronan J.E. Jr.;
 RT "Bacillus subtilis acyl carrier protein is encoded in a cluster of
 RT lipid biosynthesis genes."
 RL J. Bacteriol. 178:4794-4800(1996).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=96044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Berteiro M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter R.M.,
 RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
 RA Drenth K.D., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.D., Errington J., Fabre C., Ferrari E., Follger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallizi A., Galleon N.,
 RA Ghim S.Y., Guay B., Goffeau A., Golightly E.J., Grand G.,
 RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaert-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapides A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.N., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noack M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogilwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Serr S.J., Serr P., Shin B.S., Soldo B.,
 RA Soroichi A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassart A.,
 RA Viari A., Wamutt R., Wedler E., Wedler H., Wellenreger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasunuo K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis."
 RT Subtilis 390:249-256(1997).
 RL Nature 390:249-256(1997).
 RN [3]
 RN SEQUENCE OF 1-172 FROM N.A.
 RP STRAIN=168;
 RC MEDLINE=98195738; PubMed=9534248;
 RX Foulger D., Errington J.;
 RA "A 28 kbp segment from the spvM region of the Bacillus subtilis 168
 RT genome."
 RT Microbiology 144:801-805(1998).
 RL [4]
 RN SEQUENCE OF 230-246 FROM N.A.
 RP STRAIN=168;
 RC Oguno A., Kakeshita H., Takematsu H., Nakamura K., Yamane K.;
 RA Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 RL -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NAD(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SCD) FAMILY.
 CC -----
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CC EMBL: U99433; AAC44307.1; -
 DR EMBL: Z99112; CAB3464.1; -
 DR EMBL: Y13937; CAAT4250.1; -
 DR EMBL: D64116; BAA10974.1; -
 DR HSSP: Q12634; 1YBV.
 DR Subtilis; Bg11535; fabG.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PRO0080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; FALSE_NEG.
 DR Fatty acid biosynthesis; Oxidoreductase; NADP: Complete proteome.
 KM

```

Db      62  NPESIAVLKAITDEGGVDILVNNAGITRONLKRME-----EKSMDIENILSTIF 115
QY      127  NVIRLVAGEMGONEDOGGORGVIINTASVAEFESGOVAAVSASKGIWGLPIARDL 186
Db      116  RLKAVLARGMKK-----ROGRILVGSVGTGMNAQOANYAAKAGVIGFTKSMAREV 169
QY      187  APLGISVMTAPLEFGTPIILTSIPKENVANFLASGVFPFSRLGDPAEVAHLQATLENP-- 244
Db      170  ASAGSVYNNVYAPFETIDMTKALNDEQRATILAOVP-AGRIGDPREIASAV-ALLASPEA 227
QY      245  -PLNGEYIRLDGAIRM 259
Db      228  AYTITGELFHVNGGMYM 243

```

AC Q92506; Q90101; 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Estradiol 17 beta-dehydrogenase 8 (EC 1.1.1.62) (17-beta-HSD 8) (17-beta-hydroxysteroid dehydrogenase 8) (Kee protein) (Kee-6).
 GN HSD17B8 OR HK6 OR RING2 OR FABGL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tubby B.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 3-261 FROM N.A.
 RX MEDLINE=97001166; PubMed=8812499;
 RA Ando A., Kikuchi Y., Shigenari A., Kawata H., Okamoto N., Shima T., Chen L., Ikemura T., Abe K., Kimura M., Inoko H.;
 RT "CDNA cloning of the human homologues of the mouse Ke4 and Ke6 genes at the centromeric end of the human MNC region.";
 RL Genomics 35:600-602(1996).
 CC -1- FUNCTION: USES ESTRADIOL AS ITS PREFERRED SUBSTRATE.
 CC -1- CATALYTIC ACTIVITY: Estradiol-17-beta + NAD(P)(+) = estrone + NAD(P)H.
 CC -1- PATHWAY: BIOSYNTHESIS OF ESTROGENS.
 CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN THE LIVER AND PANCREAS, LOWER IN THE SKELETAL MUSCLE AND KIDNEY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
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 CC -----
 DR EMBL: AL031228; CAC38444.1; -
 DR EMBL: D82061; BA011529.1; -
 DR HSSP: 070351; 1E6W.
 DR Genew: HGNC:3554; HSD17B8.
 DR MIM: 601417; -
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PFO0106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Steroid biosynthesis; Oxidoreductase; NAD; Multigene family.
 FT NP_BIND 5 39 NAD (BY SIMILARITY).
 FT ACT_SITE 169 169 BY SIMILARITY.
 FT CONFLICT 117 117 E -> R (IN REF. 2).
 FT CONFLICT 193 193 R -> P (IN REF. 2).
 FT CONFLICT 208 208 Q -> K (IN REF. 2).
 FT CONFLICT 212 212 Q -> K (IN REF. 2).
 SQ SEQUENCE 261 AA; 26974 MW; 8BBB2D713171AD71 CRC64;
 Query Match 25.6%; Score 333.5; DB 1; Length 261;
 Best Local Similarity 31.2%; Pred. No. 1.1e-18;
 Matches 83; Conservative 51; Mismatches 105; Indels 27; Gaps 7;
 DB 8 VGLVAVITGASGLATAEERLVGGASAVLLDLPNSGGEAQAKL-----GN 56
 DB 9 LNSALALVYGASSGIRAVSVRLAGEGATVACDDRAAGQTVVRLKLGPGSKESPGRGN 68
 DB 57 NCVFAPADVTSEKDVOTALAKKGFGR-VDVAVNCAGIAVASKTYNKKGOTHTLEDPO 115
 DB 69 HAAF-CADYSEARAACLLLEVOYQACFSPRPVAVVSCAGITODEFLHMS-----DWD 121
 DB 116 RYLDVNLKGTFFVTRLVAGEMGONEDPGGSGVITNTSVAAFEAGGVGOAAYSAKSGI 175
 DB 122 KYIAVNLKGTFFVTRLVAGEMGONEDPGGSGVITNTSVAAFEAGGVGOAAYSAKSGI 176

DB 176 VGMTPLPARDLAPGIRKMTIAPGLFETPLLLSPKVFANFLASQVFFSRIGDPAEYAH 235
 DB 177 IGLTQTARELGRIGRINCNSVLLPFIATPMTOKVQKVKIKEMIPM-CHLGDPEVDAD 235
 DB 236 LYO--ATTEPFLNGEYIRLDGAIRM 259
 DB 236 VVAFPLASEDSGYITGTSVEVTGLFM 261
 RESULT 10
 ID FABG_VIBCH STANDARD; PRT; 244 AA.
 AC Q9K0H7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase).
 GN FABG OR VC2021.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=El Tor N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eilen J.A., Nelson W.C., Clayton R.A., Gwin M.L., Dodson R.J., Hail D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson R.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P., McDonald L., Ueberlack T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.";
 RL Nature 406:477-483(2000).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] + NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
 CC -----
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 CC -----
 DR EMBL: AE004276; AAF5169.1; ALT_INIT.
 DR HSSP: P19992; 1HDC.
 DR TIGR: VC2021; -
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PFO0106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
 FT NP_BIND 10 34 NADP (BY SIMILARITY).
 FT ACT_SITE 151 151 BY SIMILARITY.
 SQ SEQUENCE 244 AA; 25566 MW; 9FB28278BD7CC3CE CRC64;
 Query Match 25.3%; Score 330.5; DB 1; Length 244;
 Best Local Similarity 32.0%; Pred. No. 1.7e-18;
 Matches 82; Conservative 54; Mismatches 103; Indels 17; Gaps 5;
 DB 7 SVKGLVAVITGASGLATAEERLVGGASAVLLDLPNSGGEAQAKLGNCFAPADVT 66
 DB 2 NLEKVALVYGASSGIGALALAEAGAVIGTATSESGAQAISDVLGNGKGMALNVT 61
 DB 67 SEKDVOTALAKKGFGRVDVAVNCAGIAVASKTYNKKGOTHTLEDPOFVRLVNLGTF 126

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RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.,
RA "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima."
RU Nature 399:323-329(1999).
CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
CC PATHWAY.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
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CC -----
DR EMBL: AE001811; AAD36790.1;
DR HSSP: P50162; IAEI.
DR TIGR: TM1724;
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KM Fatty acid biosynthesis; Oxidoreductase; NADP: Complete proteome.
FT NP_BIND 10 34 NADP (BY SIMILARITY).
FT ACT_SITE 154 154
FT SEQUENCE 246 AA; 26401 MW; 8C08904D2609142 CRC64;
SQ
Query Match 26.3%; Score 343; DB 1; Length 246;
Best Local Similarity 33.7%; Pred. No. 1.9e-19;
Matches 86; Conservative 47; Mismatches 104; Indels 18; Gaps 5;
QY 8 VAGLVAVITGASGIGLATAERLVGGASAVLLDPNSGGA---QAQKLGNCYFAAD 64
DB 3 LERKVCILITGAASGIGKATTLTFAQEGATVAGDISKENSLSVEAGSLPEKYPVYN 62
QY 65 VTSEKDVOTALAKKRGFRVDVAVNACGIAVASKTYNKKGOTLTLEDFQVLDVNLNG 124
DB 63 VYDRODIKEVEKVKYQKGRIDVIVNNGITRDALLVRKE-----EDMDAVIVNKG 116
QY 125 TENVIRLVAGENGQNEPDGQGVYINTASYAAEAGVGQAAYSASKGIVGMLPIAR 184
DB 117 VFNVTGMVVPYMKQ-----RNGSIVNVSVVGYGNQNYAASRAGVIGMKTKAK 170
QY 185 DLAPIGIRVWTAPGLFGTPILTSLPEKVAANFLASOVPPSRIGDPAEYAHV--QATIE 242
DB 171 ELAQRIRVNAVAPGIEFTPMTEKLPKARETALSRIPLGRFGPEEVAQVILTLADBE 229
QY 243 NPLINCEVIRLDGAI 257
DB 230 SSYVTQGVIGDGL 244

RESULT 8
FABG_CUPLA STANDARD; PRT; 320 AA.
AC
P28643;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase, chloroplast precursor
DE (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase).
GN CLKR27.
OS Cuphea lanceolata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Lythraceae; Cuphea.
NCBI_TaxID=9330;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=92293104; PubMed=1376402;
RA Klein B., Pawlowski K., Hoerlcke-Grandpierre C., Schell J.,
RA Toepfer R.;
RT "Isolation and characterization of a cDNA from Cuphea lanceolata
RT encoding a beta-ketoacyl-ACP reductase."
RU Mol. Gen. Genet. 233:122-128(1992).
CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
CC PATHWAY.
CC -1- SUBUNIT: HOMOTETRAMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST AND NON-PHOTOSYNTHETIC
CC PLASTIDS.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X64566; CAA45866.1;
DR PIR: S19832; S19832.
DR HSSP: P50162; IAEI.
DR InterPro: IPR002198; ADH_short.
DR PIR: S19832; S19832.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KM Fatty acid biosynthesis; Oxidoreductase; NADP: Chloroplast;
FT TRANSIT 1 61 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 62 320
FT NP_BIND 82 106 NADP (BY SIMILARITY).
FT ACT_SITE 227 227 BY SIMILARITY.
FT SEQUENCE 320 AA; 33103 MW; 06BAF0522B8C87 CRC64;
SQ
Query Match 25.7%; Score 335; DB 1; Length 320;
Best Local Similarity 32.7%; Pred. No. 1e-18;
Matches 87; Conservative 46; Mismatches 111; Indels 22; Gaps 6;
QY 2 AAACRSYKGLVAVITGASGIGLATAERLVGGASAVLLDPNSGGA---QAQKLG 56
DB 69 AGAQSVESEPVYIYTGASRGKALALSLGKACRYLVAVASSKAEVSEIEAFGG 127
QY 57 NCVFAPADVTESEKDVOTALAKKRGFRVDVAVNACGIAVASKTYNKKGOTLTLEDFOR 116
DB 128 QALTFGGDVSKEDVEAMIKTAVDAKGTIVIVNNAITDGLMKRKSQ-----WQE 181
QY 117 VLDVNLNGTENVIRLVAGENGQNEPDGQGVYINTASYAAEAGVGQAAYSASKGIV 176
DB 182 VIDNLTLGVFLCTQAAKIMKK-----KKGRILINIASVVGIVGNAGQANTSAKAGVI 235
QY 177 GMTLPIADLAPIGIRVWTAPGLFGTPILTSLPEKVAANFLASOVPPSRIGDPAEYAHV 236
DB 236 GFTIVAREYASRNINNAVAPGISISSDMTSKGLDDINKKILLETIPLGRYGQPEEVA 294
QY 237 VQALLENP---FLNGEYVIRLDGAI 259
DB 295 VEFLLAINPASSYVVGQVFTIDGGMT 320

RESULT 9
DDB8_HUMAN STANDARD; PRT; 261 AA.
ID DDB8_HUMAN

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DR EMBL: AE003507; AAF48797.1;
DR HSSP: O70351; 1E6W.
DR FlyBase; FBgn0021765; scu.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NAD; Mitochondrion.
FT NP_BIND 6 31 NAD (BY SIMILARITY).
FT ACT_SITE 162 162 BY SIMILARITY.
FT MUTAGEN 33 33 L->Q; LEUHAL ALLELE.
FT MOTIF 120 120 F->I; LEUHAL ALLELE.
SQ SEQUENCE 255 AA; 26905 MW; F58690643FA0FD03 CRC64;

Query Match
Best Local Similarity 69.8%; Score 910; DB 1; Length 255;
Matches 175; Conservative 29; Mismatches 50; Indels 0; Gaps 0;

QY 8 VKGLVAVITGASGLGATAEELVGGASAVLLDLPNSGGGAQAKKLGNNCEPAPDVT 67
DB 2 IKNAVSLVTGASGSGRAETAEELVGGASAVLLDLPNSGGGAQAKKLGNNCEPAPDVT 61
QY 68 EKDVQALALAKGKGRVAVNAGIAVASKTYNLKGGTHTLEDFORVLDVNLGTFN 127
DB 62 EKDVSAALQTAQKDFGRDLVYNCAGITFAKTENPKNAHRLDEDFORVINTVGTEN 121
QY 128 VIRLVAGEMQNEPDQGGGVIIINTASVAPEGOVGOAAYASASKGIVGMLPIARDLA 187
DB 122 VIRLVAGEMQNEPDQGGGVIIINTASVAPEGOVGOAAYASASKGIVGMLPIARDLA 181
QY 168 PLGIVMTIAGLTFETPLTSLPEKVNANFLASQVPEPRIGDDPAEYAHVQALIEEPLN 247
DB 162 TGGINICITAPLEFTPTMALPEKVRTEFLAKSTIPFORLEPSEYAHVQALIEEPLN 241
QY 248 GEVIRLDGAIKMP 261
DB 242 GEVIRLDGAIKMP 255

RESULT 6
YD50_MTCUTU STANDARD: PRT; 247 AA.
ID YD50_MTCUTU
AC Q11020;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative oxidoreductase Ry1350 (EC 1.-.-.-).
GN FABG2 OR RV1350 OR MT1393 OR MTCY02B10.14.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeyer K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jorgels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Ruster J.E., Taylor K., Whitehead S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,

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RA Delcher A., Uitterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains";
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
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CC -----
DR EMBL: Z75555; CAAG9983.1;
DR EMBL: AE007012; AAK45656.1;
DR HSSP: O70351; 1E3S.
DR TIGR; MT1393;
DR Tuberculist; RV1350;
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
FT NP_BIND 9 34 NAD (BY SIMILARITY).
FT ACT_SITE 155 155 BY SIMILARITY.
SQ SEQUENCE 247 AA; 25871 MW; 76CA07892E7BBA73 CRC64;

Query Match
Best Local Similarity 29.3%; Score 382.5; DB 1; Length 247;
Matches 96; Conservative 43; Mismatches 91; Indels 17; Gaps 5;

QY 13 AVITGASGGLGATAEELVGGASAVLLDLPNSGGGAQAKKLGNN--CYFAPADVTSEKD 70
DB 10 AVITGASGGLGATAEELVGGASAVLLDLPNSGGGAQAKKLGNN--CYFAPADVTSEKD 69
QY 71 VQTRALAKGKGRVAVNAGIAVASKTYNLKGGTHTLEDFORVLDVNLGTFNVR 130
DB 70 VQTRALAKGKGRVAVNAGIAVASKTYNLKGGTHTLEDFORVLDVNLGTFNVR 123
QY 131 LVAGEMQNEPDQGGGVIIINTASVAPEGOVGOAAYASASKGIVGMLPIARDLAPIG 190
DB 124 LVAGEMQNEPDQGGGVIIINTASVAPEGOVGOAAYASASKGIVGMLPIARDLAPIG 177
QY 191 IRVVTIAPGLEFTPLTSLPEKVNANFLASQVPEPRIGDDPAEYAHVQALIEE--NPEFLG 248
DB 178 IRVVTIAPGLEFTPLTSLPEKVNANFLASQVPEPRIGDDPAEYAHVQALIEE--NPEFLG 236
QY 249 EVIRLDG 255
DB 237 TVLDVTC 243

RESULT 7
FABG_THEMEA STANDARD: PRT; 246 AA.
ID FABG_THEMEA
AC Q9X248;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
DE acyl carrier protein reductase).
GN FABG OR TM1724.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogae (class); Thermotogales;
OC Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
 OC NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X GBA.
 RA Fu J., Chen X., Stern D., Yan S.D.;
 RA Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA
 CC + NADH;
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
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 CC -----
 CC EMBL: U96116; AAB57689.1; ALT_INIT.
 CC DR HSSP: C070351; 1E6W.
 CC DR SWISS-2DPAGE: C08756; M0USE.
 CC DR MGD: MG1:133871; Hsd17D10.
 CC DR InterPro: IPR002198; ADH_short.
 CC DR Pfam: PF00106; adh_short.1.
 CC DR PRINTS: PRO0080; SDRFAMILY.
 CC DR PROSITE: PS00061; ADH_SHORT; 1.
 CC KM Oxidoreductase; NAD.
 CC FT NP_BIND 12 37 NAD (BY SIMILARITY).
 CC FT ACT_SITE 168 168 BY SIMILARITY.
 CC SO SEQUENCE 261 AA; 27418 MW; 61213B13E283D41 CRC64;
 Query Match 87.0%; Score 1134; DR 1; Length 261;
 Best Local Similarity 86.2%; Pred. No. 6.3e-80;
 Matches 225; Conservative 19; Mismatches 17; Indels 0; Gaps 0;
 QY 1 MAACRSVAGLVAVITGASGLATAEVLVVGAGSAYLLDLPNSGGENAOKKIGNCF 60
 DB 1 MAANVSAGLVAVVVGASGPMWAKTAKLVGGAFAVLDPDESGEQAOKKIGESCIF 60
 QY 61 AAPADVTSEKDVQATLALAKGRGRDVAVNCGIYASTYKLGQHTTLEDPQRYDV 120
 DB 61 AAPAVTSEKEIQAAITLAEKFGRIIDVAVNCGIYASTYKLGQHTTLEDPQRYDV 120
 QY 121 NMGTGTVRLVAGENGNEPDGQGGVYINTASVAFEGVGQAAYSASRKGIVGML 180
 DB 121 NLGTGTVRLVAGENGNEPDGQGGVYINTASVAFEGVGQAAYSASRKGIVGML 180
 QY 181 PIARDIAPGIRVMTAPGLGTPPLTSPKAVANFLAQVFPFSLGSPATYAHLYOAI 240
 DB 181 PIARDIAPGIRVMTAPGLGTPPLTSPKAVANFLAQVFPFSLGSPATYAHLYOAI 240
 QY 241 IENPFLNGEYIRLDGAIKMP 261
 DB 241 IENPFLNGEYIRLDGAIKMP 261
 RESULT 5
 ID HCD2_DROME STANDARD; PRT; 255 AA.
 AC 018404;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II NADH)
 DE (scully protein).
 GN SCU OR CG7113.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LEU-33 AND PHE-120.
 RC STRAIN=Canlon-S;
 RX MEDLINE=98252852; PubMed=9585418;
 RA Toroja L., Ottuno-Satagun D., Ferrus A., Haemmerle B., Barbás J.A.;
 RA Scully, an essential gene of Drosophila, is homologous to mammalian
 RA mtoccondrial type II L-3-hydroxyacyl-CoA dehydrogenase/amyloid beta
 RT peptide-binding protein.
 RL J. Cell Biol. 141:1009-1018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Stoughton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt J.G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolintsov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavalier S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glöckner A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ideyama C.,
 RA Jaiswal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K.A., Nuskern D.R., Paclet J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheefer F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spredler A.C., Stapleton M., Strong R., Sun E.,
 RA Switzkes R., Tector C., Turner C., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhao G., Zhao Q., Zheng L.,
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT The genome sequence of Drosophila melanogaster.
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: MAY PLAY A ROLE IN GERM LINE FORMATION.
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA
 CC + NADH.
 CC -1- SUBUNIT: MULTIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
 CC -1- TISSUE SPECIFICITY: FOUND IN MANY TISSUES INCLUDING CNS. HIGHEST
 CC EXPRESSION IN BOTH EMBRYONIC GONADAL PRIMORDIA AND MATURE OVARIES
 CC AND TESTES.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
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 CC EMBL: Y15102; CAA75377.1;

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CC EMBL; AB002156; BAA19510.1; -

DR HSSP; 070351; 1E6M.

DR InterPro: IPR002198; ADH_short.

DR Pfam: PF00106; adh_short; 1.

DR PRINTS; PR00080; SDRFAMILY.

DR PROSITE; PS00061; ADH_SHORT; 1.

KW Oxidoreductase; NAD; Mitochondrion.

FT NP_BIND 12 37 NAD (BY SIMILARITY).

FT ACT_SITE 168 168 BY SIMILARITY.

FT SEQUENCE 261 AA; 27140 MW; 8C7572B6A9A49780 CRC64;

Query Match

Best Local Similarity 92.6%; Score 1208; DB 1; Length 261;

Best Local Similarity 92.0%; Pred. No. 1,4e-85;

Matches 240; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 MAACRSVGLVAVITGASGLGATAEELVVGASAVLLDLPNSGGEAAKKGNNCF 60

DB 1 MAACRSVGLVAVITGASGLGATAEELVVGASAVLLDLPNSGGEAAKKGSCAF 60

QY 61 APADVTSEKDVQALALAKGKRGVDVAVNCAAGIVASTYVLLKKGQHTLDFQVLDV 120

DB 61 APADVTSEKDVQALALAKGKRGVDVAVNCAAGIVASTYVLLKKGQHTLDFQVLDV 120

QY 121 NLMTGFNVRILVAGKGNPEPDGGRGVYINTASVAEFGVGGAAYASASKGIYGMTL 180

DB 121 NLMTGFNVRILVAGKGNPEPDGGRGVYINTASVAEFGVGGAAYASASKGIYGMTL 180

QY 181 PIARDIAPGIRVMTAPGLFGTPLTSLPEKYANFLASQVPPPSRLGPAYAHLYQAI 240

DB 181 PIARDIAPGIRVMTAPGLFGTPLTSLPEKYANFLASQVPPPSRLGPAYAHLYQAI 240

QY 241 ENPFLNGEVIRLDGAIKMP 261

DB 241 ENPFLNGEVIRLDGAIKMP 261

RESULT 3

HCD2_RAT STANDARD; PRT; 260 AA.

ID HCD2_RAT

AC 070351: 090YD4:

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)

DE (Endoplasmic reticulum-associated amyloid beta-peptide binding protein).

GN HADH2 OR ERAB.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Gunn-Moore F.J., Tavaire J.M.;

RT "Rattus norvegicus amyloid beta-peptide binding protein (ERAB) mRNA.";

RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Brain;

RA Yang S.-Y., He X.-Y.;

RT "Molecular cloning and characterization of the cDNA of rat brain short chain L-3-hydroxyacyl-CoA dehydrogenase.";

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

RN [3]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RC TISSUE=Brain;

RA MEDLINE=20481418; PubMed=11023795;

RA Powell A.J., Read J.A., Banfield M.J., Gunn-Moore F., Yan S.D., Lustbader J., Stern A.R., Stern D.M., Brady R.L.;

"Recognition of structurally diverse substrates by type II 3-hydroxyacyl-CoA dehydrogenase (HADH II)/amyloid-beta binding protein (ABP)." J. Mol. Biol. 303:311-327(2000).

CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA + NADH.

CC -1- SUBUNIT: HOMOTETRAMER.

CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).

CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (CDR) FAMILY.

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CC EMBL; AF049878; AAC05747.1; -

DR EMBL; AF069770; AAF14853.1; -

DR PDB; 1E3W; 25-MAY-01.

DR PDB; 1E3S; 25-MAY-01.

DR PDB; 1E6W; 25-MAY-01.

DR InterPro: IPR002198; ADH_short.

DR Pfam: PF00106; adh_short; 1.

DR PRINTS; PR00080; SDRFAMILY.

DR PROSITE; PS00061; ADH_SHORT; 1.

KW Oxidoreductase; NAD; Acetylation; 3D-structure.

FT INIT_MET 0 0

FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).

FT NP_BIND 11 35 NAD (BY SIMILARITY).

FT ACT_SITE 167 167 BY SIMILARITY.

FT CONFLICT 4 4 V->C (IN REF. 2).

FT SEQUENCE 260 AA; 27114 MW; 30F7E723A95F9227 CRC64;

Query Match

Best Local Similarity 87.7%; Score 1153; DB 1; Length 260;

Best Local Similarity 87.7%; Pred. No. 2.2e-81;

Matches 228; Conservative 17; Mismatches 15; Indels 0; Gaps 0;

QY 2 AAACRSVGLVAVITGASGLGATAEELVVGASAVLLDLPNSGGEAAKKGNNCF 61

DB 1 AAACRSVGLVAVITGASGLGATAEELVVGASAVLLDLPNSGGEAAKKGNNCF 60

QY 62 PADVTSEKDVQALALAKGKRGVDVAVNCAAGIVASTYVLLKKGQHTLDFQVLDV 121

DB 62 PADVTSEKDVQALALAKGKRGVDVAVNCAAGIVASTYVLLKKGQHTLDFQVLDV 120

QY 121 NLMTGFNVRILVAGKGNPEPDGGRGVYINTASVAEFGVGGAAYASASKGIYGMTL 181

DB 121 NLMTGFNVRILVAGKGNPEPDGGRGVYINTASVAEFGVGGAAYASASKGIYGMTL 180

QY 182 IARDIAPGIRVMTAPGLFGTPLTSLPEKYANFLASQVPPPSRLGPAYAHLYQAI 241

DB 182 IARDIAPGIRVMTAPGLFGTPLTSLPEKYANFLASQVPPPSRLGPAYAHLYQAI 240

QY 242 ENPFLNGEVIRLDGAIKMP 261

DB 242 ENPFLNGEVIRLDGAIKMP 260

RESULT 4

HCD2_MOUSE STANDARD; PRT; 261 AA.

ID HCD2_MOUSE

AC 008756;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)

DE (Endoplasmic reticulum-associated amyloid beta-peptide binding protein).

GN HADH2 OR HSD17B10 OR ERAB.

OS Mus musculus (mouse).

HC02_HUMAN
ID HC02_HUMAN STANDARD: PRT: 261 AA.
AC 099714;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)
DE (Endoplasmic reticulum-associated amyloid beta-peptide binding protein) (short-chain type dehydrogenase/reductase XH86G2).
GN HADH2 OR ERAB OR XH962 OR SCHAD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97478528; PubMed=9338779;
RA Yan S.D., Fu J., Soto C., Chen X., Zhu H., Al-Mohanna F., Collins K., Zhu A., Stern E., Saldo T., Tohyama M., Ogawa S., Rober A., Stern D.;
RT "An intracellular protein that binds amyloid-beta peptide and mediates neurotoxicity in Alzheimer's disease.";
RL Nature 389:689-695(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhuchenko O.P., Wehnert M., Bailey J., Sun Z.S., Lee C.C.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98337980; PubMed=9671743;
RA Miller A.P., Willard H.F.;
RT "Chromosomal basis of X chromosome inactivation: identification of a multigene domain in Xp11.21-p11.22 that escapes X inactivation.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:8709-8714(1998).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98221216; PubMed=9553139;
RA He X.Y., Schultz H., Yang S.Y.;
RT "A human brain L-3-hydroxyacyl-coenzyme A dehydrogenase is identical to an amyloid beta-peptide-binding protein involved in Alzheimer's disease.";
RL J. Biol. Chem. 273:10741-10746(1998).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: BINDS INTRACELLULAR AMYLOID-BETA. BY INTERACTING WITH AMYLOID-BETA, IT MAY CONTRIBUTE TO THE NEURONAL DYSFUNCTION ASSOCIATED WITH ALZHEIMER DISEASE.
CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA + NADH.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN NORMAL TISSUES BUT IS OVEREXPRESSED IN NEURONS AFFECTED IN AD.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
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CC
CC EMBL: U96132; AAC51812.1; -
CC EMBL: U73514; AAB68938.1; -
CC EMBL: AF069134; AAC39900.1; -
CC DR EMBL: AF035555; AAC15902.1; -
CC DR EMBL: AF037438; AAC16419.1; -
CC

DR EMBL: BC000372; AAH00372.1; -
DR HSSP: Q70351; 1E3S.
DR Genew: HGNC:4800; HADH2.
DR MIM: 300256; -
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PRO0080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NAD; SHORT; 1.
FT NP_BIND 12 37 NAD (BY SIMILARITY).
FT ACT_SITE 168 168 BY SIMILARITY.
SQ SEQUENCE 261 AA; 26923 MW; 9E74F242E3B6FEF1 CRC64;
Query Match 99.7%; Score 1300; DB 1; Length 261;
Best Local Similarity 99.6%; Pred. No. 1.3e-92;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAAACRSYKGLVAVITGASGLATRELYGGASVLLDPLNSGGEQAOKLNNVF 60
DB 1 MAAACRSYKGLVAVITGASGLATRELYGGASVLLDPLNSGGEQAOKLNNVF 60
QY 61 APADVTEKDVQATLALAKGFGVDVAVNCAGIAVASKTYNLKGGTHTLEDFORVLDV 120
DB 61 APADVTEKDVQATLALAKGFGVDVAVNCAGIAVASKTYNLKGGTHTLEDFORVLDV 120
QY 121 NLMGTENVIRLVAGEMGQNEPDGQGGVLIINTASVAFEGVQQAAYSAKSGIYQMTL 180
DB 121 NLMGTENVIRLVAGEMGQNEPDGQGGVLIINTASVAFEGVQQAAYSAKSGIYQMTL 180
QY 121 NLMGTENVIRLVAGEMGQNEPDGQGGVLIINTASVAFEGVQQAAYSAKSGIYQMTL 180
DB 121 NLMGTENVIRLVAGEMGQNEPDGQGGVLIINTASVAFEGVQQAAYSAKSGIYQMTL 180
QY 181 PIARDIAPIGIRVNTIAPGLEGTPLTSLPEKVNFTASOVPEPSRLGDAFEVAHVQAI 240
DB 181 PIARDIAPIGIRVNTIAPGLEGTPLTSLPEKVNFTASOVPEPSRLGDAFEVAHVQAI 240
QY 241 IENPFLNGEVIRLDGAIKMQP 261
DB 241 IENPFLNGEVIRLDGAIKMQP 261
RESULT 2
HC02_BOVIN
ID HC02_BOVIN STANDARD: PRT: 261 AA.
AC 002691;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH).
GN Bos taurus (Bovine).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=97214648; PubMed=9061028;
RA Furuta S., Kobayashi A., Miyazawa S., Hashimoto T.;
RT "Cloning and expression of cDNA for a newly identified isozyme of bovine liver 3-hydroxyacyl-CoA dehydrogenase and its import into mitochondria.";
RL Biochim. Biophys. Acta 1350:317-324(1997).
CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA + NADH.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
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Thu Jun 26 06:55:05 2003

us-09-931-186-20.rsp

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:19:47 ; Search time 7.83333 Seconds

(without alignments) updates/sec
1381.956 Million cells

Title: US-09-931-186-20

Sequence: 1 MAAACRSYKGLVAIVITGAS.....ENPLNGEVIRLDGIRMQP 261

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1300	99.7	261	1	HCD2_HUMAN
2	1208	92.6	261	1	HCD2_BOVIN
3	1153	88.4	260	1	HCD2_RAT
4	1134	87.0	261	1	HCD2_MOUSE
5	910	69.8	255	1	HCD2_PROME
6	382.5	29.3	247	1	YD50_MYCTU
7	343	26.3	246	1	FABG_THEMA
8	335	25.7	320	1	FABG_CUPLA
9	333.5	25.6	261	1	FABG_HUMAN
10	330.5	25.3	244	1	FABG_VIBCH
11	315.5	24.2	260	1	DHBB_MOUSE
12	313.5	24.0	247	1	FAGI_SYNY3
13	311.5	23.9	246	1	FABG_BACSU
14	305	23.4	260	1	YK02_MYCTU
15	302	23.2	255	1	2BHD_STREX
16	296.5	22.7	548	1	Y4V1_RHISN
17	293.5	22.5	244	1	FABG_VIBHA
18	292.5	22.4	248	1	FABG_AOUAE
19	292	22.4	249	1	BA71_EUBSP
20	292	22.4	244	1	FABG_ECOLI
21	291.5	22.4	244	1	UCPA_SALTY
22	288	22.1	263	1	PHBB_ALCEU
23	287.5	22.0	246	1	PHAB_ACISP
24	285.5	21.9	244	1	FABG_SALTY
25	284.5	21.8	256	1	Y019_THEMA
26	283.5	21.7	246	1	NODG_ACOBR
27	282	21.6	259	1	CMPE_PSEPU
28	281.5	21.6	248	1	FABG_CHLMU
29	281	21.5	250	1	LINC_PSEPA
30	279.5	21.4	241	1	PHBB_ZOORA
31	278.5	21.4	289	1	YHDF_BACSU
32	277	21.2	246	1	PHBB_CARVI
33					P45375 chromatium

RESULT 1

ALIGNMENTS

DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase.
GN FABG OR ALR1894.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Matanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
DR EMBL, AP003587; BAB73593.1; "
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR01092; HLH_basic.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 251 AA; 26218 MW; 57D0712F8EA6B698 CRC64;

Query Match 25.7%; Score 334.5; DB 16; Length 251;
Best Local Similarity 33.1%; Pred. No. 1.4e-15;
Matches 91; Conservative 46; Mismatches 97; Indels 41; Gaps 7;
QY 1 MAACRSYKGLVAVITGASGLGLATAEELVGGQASA-----VLDLPNSGG 47
DB 1 MAITSENLRGQAVAVTGAIRGIRALALELANYGATVYVNYASSSTADEVVAEITGAGG 60
QY 48 EAOAKKLGNNCFEADVTSEKDVOTALAKKFGRYDVAVNCAGTAVASKTYNLKKGQ 107
DB 61 EAVALK-----ADVSQVEQVDNLNGAIDKFRIDIVNNAGITRDITLLRMKP-- 109
QY 108 THTLEDFOFVLVDNIMGTFNVIKLVAGEMGQNEPDGQGRVINTASVAAFEQVQQA 167
DB 110 ---EDMOAVIDLNTGVLCITRAVSKMLKQ-----RSGRIINITSVAGOMGNPGQAN 159
QY 168 YSASKGIVGMLPIARDLAPIGIRVMTIAPGLFGTPIITSLPEKVAEFLASQVFPSPRL 227
DB 160 YSAKAGVIGFTKYAKELASRGITVNAVAPGFTATDNTSNLK---SEGILQYIFL-GRY 215
QY 228 GDPAEYAHVQAIENP---FLNGEVIRLDGAIRM 259
DB 216 GQPEIAGVRFELADPAAAVITGQVFNVVDGMYV 250

Search completed: June 23, 2003, 14:32:48
Job time : 32.6667 secs

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QY 128 VIRLVAGMGONEDPOGQROVITNTASVAAFEGOVGAAYASAKSGITVGTLPDIARDLA 187
DB 121 VIKFASKMIRK-----RKGRINISSVGMVGQANYAASAGITIGTKSVAKELA 174
QY 188 PIGIVMTIAPGLFETPLTSLPEKVANFLASOVFPSPRLDPAEYAHVVO--AIENPF 245
DB 175 SRGITVANAAPROFITDITDITNWLKEDIKAMKSIPL-KRAKPEEVAEVAFLASASDY 233
QY 246 LNGEVIRLDGAI RM 259
DB 234 ITGVINVDGGMV 247

RESULT 23
QY 09KA03 PRELIMINARY: PRT; 246 AA.
ID 09KA03
AC 09KA03:
DI 01-OCT-2000 (TREMblrel. 15, Created)
DI 01-OCT-2000 (TREMblrel. 15, last sequence update)
DI 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE 3-oxoacyl-lacyl-carrier protein) reductase (EC 1.1.1.100).
GN FABG OR BR2491.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_Taxid=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125/JCM 9153;
RX MEDLINE=20512582; PUBMED=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fujii F., Hirata C., Nakamura Y., Ogasawara N., Kihara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis."
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL: AF001515; BAB06210.1; -.
DR HSSP: P19992; IHDC.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; UNKNOWN.1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 246 AA; 26126 MW; 852B95EB9DEB9E90 CRC64;

Query Match 25.7%; Score 335.5; DB 16; Length 246;
Best local Similarity 34.2%; Pred. No. 1.2e-15;
Matches 90; Conservative 42; Mismatches 102; Indels 29; Gaps 7;

```

```

RESULT 24
QY 042774 PRELIMINARY: PRT; 297 AA.
ID 042774
AC 042774:
DI 01-JUN-1998 (TREMblrel. 06, Created)
DI 01-JUN-1998 (TREMblrel. 06, last sequence update)
DI 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE 3-oxoacyl-lacyl-carrier protein)-reductase.
GN OAR-1 OR B2A19.180.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_Taxid=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Buerger F., Brois B., Weiss H.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Schulte U., Altm V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL: AF042860; AAB99799.1; -.
DR EMBL: AL380092; CAB98248.1; -.
DR HSSP: O70351; 1B6W.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Oxidoreductase.
SQ SEQUENCE 297 AA; 31342 MW; 8DC08FEDF584196F CRC64;

Query Match 25.7%; Score 335.5; DB 3; Length 297;
Best local Similarity 31.7%; Pred. No. 1.5e-15;
Matches 97; Conservative 39; Mismatches 103; Indels 67; Gaps 8;

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RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 15692 / PAOI;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Ewlan A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.D., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garner R.L., Goltzer L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Laidig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reiter J., Salter M.H., Hancock R.E.W., Lory S., Olson M.V.,
RT "Complete genome sequence of *Pseudomonas aeruginosa* PAOI, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC EMBL: AE004854; ANG0777.1; -
DR HSSP: PS0163; 2AEI.
DR InterPro: IPR002198; ADH_short.
DR InterPro: IPR001064; Crystalin.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR Oxidoreductase; Complete proteome.
KW SEQUENCE 252 AA; 26720 MW; F1F445AB82C2D8DE CRC64;
SQ
Query Match 27.2%; Score 355; DB 16; Length 252;
Best Local Similarity 35.18; Pred. No. 5.7e-17;
Matches 94; Conservative 40; Mismatches 100; Indels 34; Gaps 7;
QY 8 VKGLVAVITGASGLGATAEERLVGQASAVLLDLPN-----SGGEAQAKKIG 55
DB 3 LMKVAVITGGCGGGRAMGEYLAGARLALVDNRERLDEAVAACKAAGDARA---- 58
QY 56 NNCVFAPADYTSKDVQTLALAKGFGVADVAVNCAGIYASVSKYINLKGGTH--TLED 113
DB 59 ----YVCNVADEQVTHVAQVADFGAINGLVNNAIGLRDLGTLTKVAGDLSKKSLAQ 113
QY 114 FQRLVDVNLMTGFENVTIRLVAGEMGQ--NEPDGGGGRGVYINTASVAFEGQVQQAAYSAS 171
DB 114 MOSVIDVNLGVLCRREVAAKMIELKNE-----GALVNSSISR-AGNNGQANYSA 165
QY 172 KGSIVGKTLPIADLPITGRVTTIAPGLFGPILTSLEKYANFLASQVPPSRGDA 231
DB 166 KAGVADDTVMKELARKYGRVAGVAPGTEEMTKAGMEALEKKTAGIPL-KRGKTV 224
QY 232 EYAHVQATENPFLNGEVRILDGAR 259
DB 225 EIAHSAVIFENDYYGRVLELDGGR 252

RESULT 21

Q97DA6 PRELIMINARY; PRT; 249 AA.
ID Q97DA6;
AC Q97DA6;
DT 01-OCT-2001 (TREMblrel. 18, Created)
DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE 3-Ketoacyl-acyl carrier protein reductase.
GN CAC3574.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_Taxid=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R.L., Lee H.M., Dubois J., Qiu D., Hilti Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.,
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium *Clostridium acetobutylicum*."
RL J. Bacteriol. 183:4823-4838(2001).

DR EMBL: AE007854; AAK81497.1; -
DR InterPro: IPR002198; ADH_short.
DR InterPro: IPR001092; HLH_basic.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
DR Complete proteome.
KW SEQUENCE 249 AA; 26247 MW; B13D7EDAC21A626A CRC64;
SQ
Query Match 26.5%; Score 345.5; DB 16; Length 249;
Best Local Similarity 33.28; Pred. No. 2.5e-16;
Matches 86; Conservative 56; Mismatches 96; Indels 21; Gaps 6;
QY 8 VKGLVAVITGASGLGATAEERLVGQASAVLLDLPNSGGEAQ-----AKKIGNCVFAP 62
DB 5 LSGVAVVVTGAGRGLAGRAIALKLAEGANLV-VNYSSEAEETQRLKEIELESGKAAVAK 63
QY 63 ADVTSKDVQTLALAKGFGVADVAVNCAGIYASVSKYINLKGGTHLEDFOVRLDVNL 122
DB 64 ADISKYDEAETIKKALDEGVYDILVNNAGITKDNILMKKE-----EDPSVINVL 117
QY 123 MGFENVIRLVAGEMGQNEPDGGGVYINTASVAFEGQVQQAAYSASKGIYGMTLP 182
DB 118 KGAFCNCKIKHTSRVNLK-----KSGKITINISSVIGLGNAGQVNYAAKAGIIGMTKSV 171
QY 183 ARDLAPIGIRMTIAPGLFGPILTSLEKYANFLASQVPPSRGDAEYAHVQAT 242
DB 172 AKELASRITVNAAPGITSMDTLTKORSEIVAAVPL-NKVGAEADVANLVFLAS 230
QY 243 --NEFLNGEVRILDGAR 259
DB 231 DLSVITGQVINVDDGMV 249

RESULT 22
Q989W0 PRELIMINARY; PRT; 247 AA.
ID Q989W0;
AC Q989W0;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Dehydrogenases with different specificities (related to short-chain
DE alcohol dehydrogenases).
GN FABG3 OR TTE1472.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_Taxid=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-M847 / JCM11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong X., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.,
RT "A complete sequence of *T. tengcongensis* genome."
RL Genome Res. 12:689-700(2002).
DR EMBL: AE013105; AAM24694.1; -
KW Complete proteome.
SQ SEQUENCE 247 AA; 26606 MW; 357D82B8C60E7947 CRC64;
SQ
Query Match 26.0%; Score 339.5; DB 16; Length 247;
Best Local Similarity 34.3%; Pred. No. 6.4e-16;
Matches 87; Conservative 48; Mismatches 100; Indels 19; Gaps 6;
QY 12 VAVITGASGLGATAEERLVGQASAVLLDLPN--SGGEA--QAKKIGNCVFAPADYTS 67
DB 7 VAFVVGSGSIGIRALVARKGFIATYYKDDSAEEVVEYKHCVDALAKCDVSK 66
QY 68 EKDVOFATALAKGFGVADVAVNCAGIYASVSKYINLKGGTHLEDFOVRLDVNLMTGF 127
DB 67 YEHEKAVKVIIEEGSIDVYVNNAGITKDNILMKEE-----BEMQVIDVNLKGAFFN 120

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Db      8 AVITGMXXRXRAGRPAPRRPL----ARSALEIDINDKGAAYAGLCAADKARFRNNVNS 63
OY      67 SEKDVOATALAKGKRGVDAVAVNCAGIAVASKTYNLKGGOTHTLEDFORVLDVNLKGT 126
Db      64 DEAAATTAIDQAHDLGLGNVAMNCAGILGAGRV--LKEGPMPLAGOGTVMVNLVGSF 121
OY      127 NTIRLVAGMGONEPDQSGQRCVYIINTSVAAFEQVGOAASASAKGIVGKTLPIADL 186
Db      122 NYAKAAANRMOHNEAGTDERGVYIINTASIAVEGOIQAAVYASKGVSMTLPMAREL 181
OY      187 APGIRVMTIAPGLFETPLTSLPEKV 213
Db      182 SRGIRVNTIAPGVFTPMVDMPEKV 208

RESULT 18
O8XHL1  PRELIMINARY; PRT; 246 AA.
ID      08XHL1
AC      01-MAR-2002 (TREMblrel. 20, Created)
DT      01-MAR-2002 (TREMblrel. 20, Last sequence update)
DE      3-oxoacyl-[acyl-carrier-protein] reductase.
GN      FABG OR CPE1070.
OS      Clostridium perfringens.
OC      Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC      Clostridiales; Clostridaceae; Clostridium.
OX      NCBI_TaxID=1502;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=13 / TYPE A;
RX      PubMed=11792842;
RA      Shimizu T., Ohtani K., Hirakawa H., Oshima K., Hayashita A.,
RA      Shiba T., Ogasawara N., Hattori M., Kubara S., Yamasaki H.;
RT      Complete genome sequence of Clostridium perfringens, an anaerobic
RT      flesh-eater.
RL      Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR      EMBL; AP003189; BAB80776.1;
DR      InterPro; IPR002198; ADH_short.
DR      Pfam; PF00106; adh_short; 1.
DR      PRINTS; PR00080; SDRFAMILY.
DR      PROSITE; PS00061; ADH_SHORT; 1.
KW      Complete proteome.
SQ      SEQUENCE 246 AA; 26267 MW; CD90B8C650EC817 CRC64;

Query Match      28.8%; Score 375.5; DB 16; Length 246;
Best Local Similarity 35.8%; Pred. No. 2,1e-18;
Matches 93; Conservative 47; Mismatches 97; Indels 23; Gaps 7;

OY      8 VKGLAVITGGASGLGATAEERLVGGASAVLLDLNSGGEQAOKL-----GNNCVFAP 62
Db      2 LKCKVAIVTGGTIGIRALALKLADGAN-IVINRNSKEAEELAILIEKGVKLVTK 60
OY      63 ADVTSEKDVOATALAKGKRGVDAVAVNCAGIAVASKTYNLKGGOTHTLEDFORVLDVNL 122
Db      61 CDSINFEDESKNLMDCQKEYGKIDILVNNAGITKDLIMRKE-----EDFNVADVNL 114
OY      123 MGTFFNVIRLVAGMGONEPDQSGQRCVYIINTSVAAFEQVGOAASASAKGIVGKTLPI 181
Db      115 KGTFFNKAHSAIMLK-----QRFKGIINMTSVYVGIAGNAGVYVSASKAGVIGLTRS 167
OY      182 IARDLAPIGIRVMTIAPGLFETPLTSLPEKVANFLASOVPEFSRLGDDPVEYAHLYQAT 241
Db      168 LAKELSRGITLVAVAPGFTINTMTASLSKYEESKNIPL-KRLGDEPDVAVNLVGFILA 226
OY      242 ENP--FLNGEIVRLDGAIRM 259
Db      227 SDAANYITGOVINVDGGMV 246

RESULT 19
O99YD6  PRELIMINARY; PRT; 244 AA.
ID      O99YD6

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AC      O99YD6;
DT      01-JUN-2001 (TREMblrel. 17, Created)
DT      01-JUN-2001 (TREMblrel. 17, Last sequence update)
DE      01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE      Putative beta-ketoacyl-ACP reductase (EC 1.1.1.100).
GN      FABG OR SPY1749.
OS      Streptococcus pyogenes.
OC      Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC      Streptococcaceae; Streptococcus.
OX      NCBI_TaxID=1314;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;
RX      MEDLINE=21192684; PubMed=11296296;
RA      Ferretti J.J., Moshan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA      Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lal H.S., Lin S.P.,
RA      Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA      Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT      Complete genome sequence of an M1 strain of Streptococcus pyogenes.
RT      Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
CC      -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC      (SDR) FAMILY
CC      EMBL; AE006603; AAK34493.1;
DR      HSSP; P50162; IAB1.
DR      InterPro; IPR002198; ADH_short.
DR      InterPro; IPR001092; HLH_basic.
DR      Pfam; PF00106; adh_short; 1.
DR      PRINTS; PR01608; BACINVASINC.
DR      PRINTS; PR00080; SDRFAMILY.
DR      PROSITE; PS00061; ADH_SHORT; 1.
DR      PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
KW      Oxidoreductase; Complete proteome.
SQ      SEQUENCE 244 AA; 26002 MW; 67ECE23870D40D65 CRC64;

Query Match      27.4%; Score 357.5; DB 16; Length 244;
Best Local Similarity 35.4%; Pred. No. 3,7e-17;
Matches 92; Conservative 41; Mismatches 102; Indels 25; Gaps 5;

OY      8 VKGLAVITGGASGLGATAEERLVGGASAVLLDLNSGGEQAOKL-----GNNCVFAP 60
Db      3 IKGKNIFFITGSRIGLMAHQFASLEANIYV-----NGRSALISEELVASTFDGVVVT 57
OY      61 APADVTSEKDVOATALAKGKRGVDAVAVNCAGIAVASKTYNLKGGOTHTLEDFORVLDV 120
Db      58 ISGDVSEASEAKRMVNEAIESIGSIDVLYNNAGIT-----NDKLMKMTSEDERVYIKI 111
OY      121 MGTFFNVIRLVAGMGONEPDQSGQRCVYIINTSVAAFEQVGOAAYASAKGIVGKTL 180
Db      112 NLGAFNMTQSVL-----KPIKARQGAIIINVS SVGLTGNICQANYAASKACMIGFTK 165
OY      181 PIARDLAPIGIRVMTIAPGLFETPLTSLPEKVANFLASOVPEFSRLGDDPVEYAHLYQAI 240
Db      166 SVAREVANNICVNAIAFGFIESDVTGVLPKMQEILSQIPK-KRIKAOEVAHLASF 224
OY      241 IENPFLNGEIVRLDGAIRM 260
Db      225 VEQDYITGOVTAIDGGMV 244

RESULT 20
O9HNI5  PRELIMINARY; PRT; 252 AA.
ID      O9HNI5
AC      01-MAR-2001 (TREMblrel. 16, Created)
DT      01-MAR-2001 (TREMblrel. 16, Last sequence update)
DE      01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE      Probable short-chain dehydrogenase.
GN      PA4389.
OS      Pseudomonas aeruginosa.
OC      Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC      Pseudomonas.
OX      NCBI_TaxID=287;
RN      [1]

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DB 187 MTIAPGIFETPMAGTETEVRSALAGVFPFPRRLGPDQVYALAHNIENSMNGEVIRL 246
 QY 254 DGAIRM 259
 DB 247 DGAIRM 252

RESULT 13
 ID 08UFI2 PRELIMINARY; PRT: 257 AA.
 AC 08UFI2;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE 3-hydroxyacyl-CoA dehydrogenase type II.
 GN ATU1415 OR AGC.C.2613.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608550; PubMed=11743193;
 RA Wood D.W., Setubal J.C., Kaul R., Moons D.E., Kitajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Moo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. St.,
 RA Chapman P., Clendenning J., Deatherage G., Gillet M., Grant C.,
 RA Kutyavin T., Levy R., Li M.-J., McClelland E., Palmeri A.,
 RA Raymond C., Rose G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan N., Perry M.,
 RA Gordon-Famm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Nester E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 RT C58.";
 RL Science 294:2317-2323(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194;
 RA Goodner B., Hinkle G., Gattling S., Miller N., Blanchard M.,
 RA Gourollo B., Goldman B.S., Cao Y., Askemazi M., Halling C., Mullin L.,
 RA Houmel K., Gordon J., Vaudin M., Iarchouk O., Epp A., Liu F.,
 RA Wollam C., Allinger M., Doughy D., Scott C., Lappas C., Marfeiz B.,
 RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
 RA Cleo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT Agrobacterium tumefaciens C58.";
 RL Science 294:2323-2328(2001).
 DR EMBL: AE009102; AAL42421.1; -;
 DR EMBL: AE008067; AAK87207.1; -;
 KW Complete proteome.
 SQ SEQUENCE 257 AA; 26622 MW; FF74A61FCA2B5C CRC64;

Query Match 49.4%; Score 644; DB 16; Length 257;
 Best Local Similarity 51.7%; Pred. No. 8.1e-37;
 Matches 134; Conservative 41; Mismatches 76; Indels 8; Gaps 3;

QY 7 SVKGLAVITGASGLATATERTVAGASAVLLDLPNNGGNOAKLGNNGVFAFADYT 66
 DB 2 NIEGAGALVTGAASGLGAIVARMLARGAATVTFDNGEAGKLAIEIGKAV--QGDVT 59
 QY 67 SEVDVATLALAKGKGRVDVAVNCAGIYASTYTLKKGTHLTLEDFQVRLDVNLMTG 126
 DB 60 SDDADAAIKVAASASAGGLRIIVNCAGIGTAGRI--LGRGGPQLDFEQVIRVNLIGTF 117
 QY 127 NVIRLAVAGEKGNEDPG-----GQGVIIINTASVAFAFGVGOAAVSASAKGIYGTLP 182
 DB 118 NMNRLLAAHMAEREDQGDSDRDNGVYINIASVAFEQIGQAAVAASAKGIVSLADPA 177
 QY 183 ARDLADIGIRVMTIAPGLFGLTSLPERKANFLASQVFPFSGRLGDPAEVIAHLVQAIT 242
 DB 178 ARDLAFIRIRVMTVAPGIFLTPLOGLPOVQESVSLAGIIPHSRLGDPAEFADVAFELTE 237

QY 243 NPFINGEVIRLDGAIKMP 261
 DB 238 NDYNGEVIRLDGAIKMP 256

RESULT 14
 ID 09DCX5 PRELIMINARY; PRT: 126 AA.
 AC 09DCX5;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Hydroxyacyl-coenzyme A dehydrogenase, type II.
 GN HSD17B10 OR HADH2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schmitt L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barz G.,
 RA Blake J., Boffelli D., Bojunga N., Carlini P., de Bona M.F.,
 RA Brownstein M.C., But C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hune D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seiya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Taya-Oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski B., Yoshida K., Hasegawa Y., Kanaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1. SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SCR) FAMILY.
 DR EMBL: AK002368; BAB22046.1; -;
 DR HSSP: 070351; 1B6M.
 DR MGD: MGI:1333671; Hsd17b10.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Oxidoreductase.
 SQ SEQUENCE 126 AA; 13265 MW; 78FBE6D44139989D CRC64;

Query Match 46.7%; Score 609; DB 11; Length 126;
 Best Local Similarity 95.2%; Pred. No. 8.3e-35;
 Matches 120; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 136 MGNPEPDGGGQGVINTASVAFAFGVGOAAVSASAKGIYGMFLPIARDLAPIGIRMT 195
 DB 1 MGNPEPDGGGQGVINTASVAFAFGVGOAAVSASAKGIYGMFLPIARDLAPIGIRMT 60
 QY 196 IAPGLFGLTSLPERKANFLASQVFPFSGRLGDPAEVIAHLVQAITENPFLNGEVIRLD 255
 DB 61 IAPGLFGLTSLPERKANFLASQVFPFSGRLGDPAEVIAHLVQITENPFLNGEVIRLD 120
 QY 256 AIRMP 261
 DB 121 AIRMP 126

RESULT 15
 Q8T217

RT Sinorhizobium meliloti pSyma megaplasmid.
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888 (2001).
 DR EMBL: AE007266; AAK65450.1; -.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.
 KW Plasmid; Complete proteome.
 SQ SEQUENCE 255 AA; 26329 MW; ED6C7942D3ED867C CRC64;

Query Match 51.5%; Score 672; DB 16; Length 255;
 Best Local Similarity 54.7%; Pred. No. 9.5e-39;
 Matches 139; Conservative 34; Mismatches 79; Indels 2; Gaps 1;

QY 8 VGLVAIVTGGASGLATAERLVGGASAVLLDLPNSGGEAAKILNCCVAPADYTS 67
 DB 3 LKSRFTVTVGASSGGAATVRLAOGATVGLDLKPPAGEPEPAELGAAYFRNADVTN 62
 QY 68 EKDVOTALLAKGKRGVDVAVNCAAGIYASKTYMLKKGQTHLEDFORVLDVNLMTGEN 127
 DB 63 EADATALLAFKQEGRHVAGLVNCACTAGEKI--LGSSGPHALDSFARTVAVNLIGTFN 120
 QY 128 VIRLVAGENGQNEPDGGGQGVIIINTASYAAFEQGVGAAYASKSGIVGMLPIARDLA 187
 DB 121 MIRLAEVNAGCEPDGDERGVIVNTASTAIFDQIGQAAVYASKGVAAALTLPAARELA 180
 QY 188 PIGIRMTAPGLFGTPLLTLSPKRYANFLASQVPPPSLGDPAEYAHVQAIIENPFLN 247
 DB 181 REIRIVTAPGLFGTPLLTLSPKRYANFLASQVPPPSLGDPAEYAHVQAIIENPFLN 240
 QY 248 GEYIRLDGAIKMP 261
 DB 241 GEYIRLDGAIKMP 254

RESULT 11

Q98HMA PRELIMINARY; PRT; 253 AA.

AC Q98HMA; 01-OCT-2001 (TReMBLrel. 18, Created)
 DT 01-OCT-2001 (TReMBLrel. 18, last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, last annotation update)
 DE 3-hydroxycy1-coA dehydrogenase type II.
 GN MKR2803.
 OS Rhizobium loti (Sinorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 CX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFP303099;
 RX MEDLINE=21082930; PubMed=11114968;
 RA Kaneo T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Matanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsunoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 Mesorhizobium loti";
 RL DNA Res. 7:331-338 (2000).
 DR EMBL: AP003000; BAB49842.1; -.
 DR InterPro: IPR002198; ADH_short.
 DR InterPro: IPR001092; HLH_basic.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 253 AA; 25814 MW; 8832D9EB9BD3D2A CRC64;

Query Match 51.3%; Score 669; DB 16; Length 253;
 Best Local Similarity 54.4%; Pred. No. 1.5e-38;
 Matches 137; Conservative 37; Mismatches 74; Indels 4; Gaps 2;

QY 10 GLVAIVTGGASGLATAERLVGGASAVLLDLPNSGGEAAKILNCCVAPADYTSK 69
 DB 5 GQIAIVTGGSGGSEANFARALAKGARVAFEDVIGIERAKVADIG--ISVGVDSAD 62
 QY 70 DVOTALAKGKRGVDVAVNCAAGIYASKTYMLKKGQTHLEDFORVLDVNLMTGEN 129
 DB 63 SGTAALETASKGEPRIILVNCAGIAGVGT--IGKDGPHLDQYKRVLEVNLTIGTFNMI 120
 QY 130 RLVAGENGQNEPDGGGQGVIIINTASYAAFEQGVGAAYASKSGIVGMLPIARDLAPI 189
 DB 121 RLVADRAASLEPLDGGSGGVIVNTASTAIFDQIGQAAVYASKGVGMLPIARDLAPI 180
 QY 190 GIRMTAPGLFGTPLLTLSPKRYANFLASQVPPPSLGDPAEYAHVQAIIENPFLN 249
 DB 181 GIRVITAPGLFGTPLLTLSPKRYANFLASQVPPPSLGDPAEYAHVQAIIENPFLN 240
 QY 250 VIRLDGAIKMP 261
 DB 241 TIRLDGAIKMP 252

RESULT 12

Q9AHY1 PRELIMINARY; PRT; 255 AA.

AC Q9AHY1; 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, last annotation update)
 DE FADB2x.
 GN FADB2x.
 OS Pseudomonas putida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 CX NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=U;
 RX MEDLINE=21150437; PubMed=11251808;
 RA Olivera E.R., Carnicero D., Garcia B., Minambres B., Moreno M.A.,
 RA Canedo L., DiRusso C.C., Naharro G., Llueno J.M.;
 RT "Two different pathways are involved in the b-oxidation of n-alkanoic
 and n-phenylalkanoic acids in Pseudomonas putida U: genetic studies
 and biotechnological applications";
 RL Mol. Microbiol. 39:863-874 (2001).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 (SDR) FAMILY.
 CC EMBL: AF290950; AAK18170.1; -.
 DR HSSP: O70351; 153S.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.
 KW Oxidoreductase.
 SQ SEQUENCE 255 AA; 26003 MW; 56B658DE906F73F CRC64;

Query Match 50.2%; Score 654; DB 2; Length 255;
 Best Local Similarity 54.3%; Pred. No. 1.0e-37;
 Matches 134; Conservative 40; Mismatches 70; Indels 2; Gaps 1;

QY 14 VITGASGLATAERLVGGASAVLLDLPNSGGEAAKILNCCVAPADYTSKDVCT 73
 DB 9 IVSGAAGSLGATQMLVEYAGAKMLVDLNAQVAEAKARBLGDNARAVADIDDEQAQA 68
 QY 74 ALALAKGKRGVDVAVNCAAGIYASKTYMLKKGQTHLEDFORVLDVNLMTGENVRLVA 133
 DB 69 AYDAVASAFSLQGLVNCAGIYAGERY--LGKGGPHGLASFARVAVNVLGSENLRLAA 126
 QY 134 GEMQNGNEPDGGGQGVIIINTASYAAFEQGVGAAYASKSGIVGMLPIARDLAPIRIV 193
 DB 127 AAMAGAADENGEGGVIVNTASTAIFDQIGQAAVYASKKAISLTLPAARELARIGIRV 186
 QY 194 MTIAPGLFGTPLLTLSPKRYANFLASQVPPPSLGDPAEYAHVQAIIENPFLNGEYIRL 253

OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Margenot S.,
 RA Arlet M., Billault A., Brotier P., Camus J.C., Cattolico L.,
 RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
 RA Siguer P., Thebault P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*.";
 RL Nature 415:497-502(2002).
 DR EMBL; AL646070; CAD16241.1; -
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short.1.
 DR PRINTS; P00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 KM Oxidoreductase; Complete proteome.
 SQ SEQUENCE 252 AA; 25642 MW; D6BEACDA9179DF CRC64;
 Query Match 53.0%; Score 691.5; DB 16; Length 252;
 Best Local Similarity 57.1%; Pred. No. 4,3e-40;
 Matches 145; Conservative 33; Mismatches 71; Indels 5; Gaps 3;
 QY 8 VKGLVITGASGGLTAERLVGOGASAVLLDLPNSGGEQAARKIGNCVFAPADVT 67
 DB 3 IRQVFTVIGSASGLAGTTRALAEGRVVIADLNEAGALAEITGR--FVRCDVSS 60
 QY 68 EKDVOITALAKGKRGVDVAVNCAGIAVASKTYMLKKQHTLEDFORVLDVNMGTEN 127
 DB 61 EADGQAAYOAR-SIGALAGLVNCAGIAPASRT--VGRAGPHLDQFARVININLIGFTN 117
 QY 128 VIRLVAGENGONPDGGRVYIINTASVAFAEGVGGAASASGKIYGMTPAROLA 187
 DB 118 MRLAATMTANAFNAGGERVYIINTASVAAPDGGCAVYASGSGVATLARIADS 177
 QY 188 PIGIRVMTAPGLFGLTSLPEKVANFLASQVPPSRFGDPAEYAHLYOAIENPFLN 247
 DB 178 RGIIRVMTAPGLFGLTSLPEKVANFLASQVPPSRFGDPAEYAHLYOAIENPFLN 237
 QY 248 GEVIRLDGAIRMOP 261
 DB 238 GETIRLDGAIRMOP 251
 RESULT 9
 ID 006544 PRELIMINARY; PRT; 250 AA.
 AC 006544;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Oxidoreductase, short-chain dehydrogenase/reductase family.
 GN RV1144 OR MTC165.11 OR M11177.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Gordon S.V., Eiglmeyer K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holtroyd S.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sultson J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of *Mycobacterium tuberculosis* from the
 complete genome sequence."

RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / OSEKOSH;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gynn M.U., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of *Mycobacterium tuberculosis* clinical and
 laboratory strains";
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U95584; CAB09032.1; -
 DR EMBL; AE006996; AAK45436.1; -
 DR HSSP; O70351; 1E3S.
 DR TIGR; MT1177; -
 DR TubercuList; RV1144; -
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short.1.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 KM Hypothetical protein; Complete proteome.
 SQ SEQUENCE 250 AA; 25787 MW; 123A1005A12BD66 CRC64;
 Query Match 51.6%; Score 673.5; DB 16; Length 250;
 Best Local Similarity 60.1%; Pred. No. 7,3e-39;
 Matches 152; Conservative 25; Mismatches 69; Indels 7; Gaps 4;
 QY 9 KGLVAVITGASGGLTAERLVGOGASAVLLDLPNSGGEQAARKIGNCVFAPADVT 68
 DB 4 KDAVAVVITGASGGLTATTKRLLDAGAAQVYVVD---RGDDVVGGLDPRFAQADVTDE 60
 QY 69 KDVOITALAKGKRGVDVAVNCAGIAVASKTYMLKKQHTLEDFORVLDVNMGTEN 128
 DB 61 AAVSALBELA-DSIGPARVAVVNCAGTGNATV--LSRDGVTPPLAAFKRIDINLVGFTN 117
 QY 129 IRLVAGENGONPDGGRVYIINTASVAFAEGVGGAASASGKIYGMTPAROLAP 188
 DB 118 LRLGIERIAKTEP-IGEBRGVYIINTASVAAPDGGCAVYASGSGVATLARIADS 176
 QY 189 IGIRVMTAPGLFGLTSLPEKVANFLASQVPPSRFGDPAEYAHLYOAIENPFLN 248
 DB 177 KLIRVMTAPGLFGLTSLPEKVANFLASQVPPSRFGDPAEYAHLYOAIENPFLN 236
 QY 249 EVIRLDGAIRMOP 261
 DB 237 EVIRLDGAIRMOP 249
 RESULT 10
 ID 092YSL PRELIMINARY; PRT; 255 AA.
 AC 092YSL;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Probable.
 GN RA0792 OR SMA1452.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Plasmid psyma (megaplasmid 1).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396509; PubMed=11481432;
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
 RA Bartlett M.J., Bowser L., Capela D., Galibert F., Gouzy J.,
 RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
 RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
 RA Yen K.C., Davis R.W., Federspiel N.A., Long S.R.;
 RT "Nucleotide sequence and predicted functions of the entire

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QY 123 MGFTFVIRLVAGMGONPEPDGORGVIINTASVAAPFEGOVGOAAYASASKGIVGMTLPI 182
DB 120 LGFTFVIRLVAGMGONHEKDGANGORGVIINTASVAAPFEGOVGOAAYASASKGIVGMTLPI 179
QY 183 ARDLAPIGIRVMTIAPGLFETPLTSLPEKVANFLASOVPPFSRIGDPAEYAHVQAIIE 242
DB 180 ABDFADGIRFMTIAPGLFETPLTSLPEKVASFLAQLIPNSRLGHPHEYGALVQHIIE 239
QY 243 NPFLNGEVRILDGAI RM 259
DB 240 NOYLNGEVRILDGAI RM 256

RESULT 6
Q910T0 PRELIMINARY; PRT; 255 AA.
ID 0910T0;
AC 0910T0;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2002 (TRENBLrel. 16, Last sequence update)
DE 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Probable short-chain dehydrogenase.
GN PA2354.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAOI.
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Huffnagle W.O., Kowalik D.J., Lagrou Y.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wagman S., Yan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Laidig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saiter M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL: AE004683; AAC05942.1; -.
DR HSSP: OT0351; 1E36
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Oxidoreductase; Complete proteome.
SQ
SEQUENCE 255 AA; 26426 MW; EB8FF28712D2936D CRC64;

Query Match 55.4%; Score 722; DB 16; Length 255;
Best Local Similarity 57.5%; Pred. No. 3.5e-42;
Matches 145; Conservative 39; Mismatches 66; Indels 2; Gaps 1;

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RESULT 7
Q8YBS0 PRELIMINARY; PRT; 255 AA.
ID 08YBS0;
AC 08YBS0;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE 3-oxoacyl-(acyl-carrier protein) reductase (Ec 1.1.1.100).
GN BME10816.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688;
RA Delvecchio V.G., Kapatal V., Redkar R.J., Patra G., Mujer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lydids A., Reznik G.,
RA Jalonoski L., Larsen N., D'Souza W., Bernal A., Mazur M., Goldsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Teveson J.J.,
RA Haselkorn R., Kyrides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis."
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR EMBL: AE009715; AAL54058.1; -.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Oxidoreductase; Complete proteome.
SQ
SEQUENCE 255 AA; 26263 MW; SCF61D4B37FEB730 CRC64;

Query Match 54.7%; Score 713; DB 16; Length 255;
Best Local Similarity 57.1%; Pred. No. 1.5e-41;
Matches 144; Conservative 37; Mismatches 69; Indels 2; Gaps 1;

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RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glassi C., King B., Kochia H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Staudt F., Suzuki K., Tomita K., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balarelli R., Barsh G.,
 RA Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
 RA Morone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata T., Storch K.F.,
 RA Suzuki K., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDS) FAMILY
 DR EMBL: AK013340; BAB28800.1; -
 DR HSSP: O70351; IE6W.
 DR MGD: MGI:133871; Hsd17b10.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR OXIDOREDUCTASE.
 KW OXIDOREDUCTASE.
 SQ SEQUENCE 261 AA; 27273 MW; F36CD19C7FCEFAF CRC64;

Query Match 88.6%; Score 1155; DB 11; Length 261;
 Best Local Similarity 87.4%; Pred. No. 6.4e-72;
 Matches 228; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

QY 1 MAACSVKGLVAVITGGASGLATAEPLVGGASAVLLDLPNSGGEQAOKLGNCF 60
 DB 1 MAALVSVKGLVAVITGGASGLATAEPLVGGASAVLLDLPNSGGEQAOKLGNCF 60
 QY 61 APADVSEKDVOTALALAKGFGVAVNCAIGAVASTYVNLKKGOTITLDFORVLDV 120
 DB 61 APANVSEKIOALALAKGFGRIDVAVNCAIGAVASTYVNLKKGOTITLDFORVLDV 120
 QY 121 NLMGTRVITLVAGENGONPDGQGVITINTASVAEEGQGAASASGQVGM 180
 DB 121 NLMGTRVITLVAGENGONPDGQGVITINTASVAEEGQGAASASGQVGM 180
 QY 181 PIRADLPAGIRVMTAPGLFGTPLTSLPEKAVNPLASQVPPSRGPAEVAHLVCAI 240
 DB 181 PIRADLPAGIRVMTAPGLFGTPLTSLPEKAVNPLASQVPPSRGPAEVAHLVCAI 240
 QY 241 IENPFLNGEYIRLDGAIKMP 261
 DB 241 IENPFLNGEYIRLDGAIKMP 261

RESULT 4
 O8TCV9 PRELIMINARY; PRT; 196 AA.
 AC O8TCV9;
 DT 01-JUN-2002 (TEMBLrel. 21, Created)
 DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
 DE Endoplasmic reticulum-associated amyloid beta peptide-binding protein
 DE (Fragment).
 GN ERB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Deininger M.H., Meyermann R., Schluesener H.U.;
 RT "Expression, release and induction of endoplasmic reticulum-associated
 RT amyloid beta-binding protein in brain disease."
 RT submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY092415; AAM18189.1; -
 FT NON-TER 1
 FT 196
 SQ SEQUENCE 196 AA; 20581 MW; 240DE19665A6A CRC64;
 Query Match 75.5%; Score 984; DB 4; Length 196;
 Best Local Similarity 99.5%; Pred. No. 2.6e-60;
 Matches 195; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 51 AKKGNVCVPAADVTSEKDVOTALALAKGFGVAVNCAIGAVASTYVNLKKGOTHT 110
 DB 1 AKKGNVCVPAADVTSEKDVOTALALAKGFGVAVNCAIGAVASTYVNLKKGOTHT 60
 QY 111 LEDEFORVLDVNLGTFENVIRLVAGENGONPDGQGVITINTASVAEEGQGAAYSA 170
 DB 61 LEDEFORVLDVNLGTFENVIRLVAGENGONPDGQGVITINTASVAEEGQGAAYSA 120
 QY 171 SKGIVGKTLPIADLPAGIRVMTAPGLFGTPLTSLPEKAVNPLASQVPPSRGDP 230
 DB 121 SKGIVGKTLPIADLPAGIRVMTAPGLFGTPLTSLPEKAVNPLASQVPPSRGDP 180
 QY 231 AEVAHLVCAIENPFL 246
 DB 181 AEVAHLVCAIENPFL 196

RESULT 5
 Q19102 PRELIMINARY; PRT; 258 AA.
 AC Q19102;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
 DE Probable 3-hydroxyacyl-CoA dehydrogenase F01G4.2 type II (EC 1.1.1.35)
 DE (Type II HADH).
 DE F01G4.2.
 GN Caenorhabditis elegans.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodermidae; Caenorhabditis.
 OX NCBI_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Harris B.;
 RL Submitted (Jan-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: L-3-HYDROXYACYL-COA + NAD(+) = 3-OXOACYL-COA +
 CC NADH.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC FAMILY (SDS).
 DR EMBL: Z68341; CAA92764.1; -
 DR HSSP: O70351; IE6W.
 DR WormPep: F01G4.2; CE03127.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR Hypothetical protein; Oxidoreductase; NAD; Mitochondrion.
 KW Hypothetical protein; Oxidoreductase; NAD (BY SIMILARITY).
 FT ACT_SITE 165
 FT NP_BIND 165
 FT AC_SITE 165
 SQ SEQUENCE 258 AA; 27143 MW; 86BF2568EE6902B3 CRC64;

Query Match 57.5%; Score 750; DB 5; Length 258;
 Best Local Similarity 59.9%; Pred. No. 4.2e-44;
 Matches 154; Conservative 34; Mismatches 67; Indels 2; Gaps 1;

QY 3 AACRSVKGIVAVITGGASGLATAEPLVGGASAVLLDLPNSGGEQAOKLGNVCVAP 62
 DB 2 SALRSTKGLVAVITGGASGLATAEPLVGGASAVLLDLPNSGGEQAOKLGNVCVAP 59
 QY 63 AAVTSEKDVOTALALAKGFGVAVNCAIGAVASTYVNLKKGOTITLDFORVLDVNL 122
 DB 60 AAVTSEKDVOTALALAKGFGVAVNCAIGAVASTYVNLKKGOTITLDFORVLDVNL 119

90 286.5 22.0 246 2 09RB80
 91 286.5 22.0 246 2 09F519
 92 286.5 22.0 256 17 09RT15
 93 286 21.9 252 16 09ZPPO
 94 285.5 21.9 257 16 09WYD3
 95 285 21.9 255 16 09PCQ2
 96 285 21.9 317 10 09X68
 97 284.5 21.8 253 16 09CH41
 98 284.5 21.8 272 16 09R81
 99 284 21.8 275 16 09K40
 100 283 21.7 258 16 09X89

ALIGNMENTS

RESULT 1
 Q96HD5 PRELIMINARY; PRT; 252 AA.
 AC Q96HD5;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
 DE Similar to hydroxycyl-coenzyme A dehydrogenase, type II.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
 CC EMBL; BC008708; AA08708.1; -;
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.
 KM Oxidoreductase.
 SQ SEQUENCE 252 AA; 25984 MW; F36B371070CE872D CRC64;

Query Match

Best Local Similarity 96.2%; Score 1241.5; DB 4; Length 252;
 Matches 251; Conservative 0; Mismatches 1; Indels 9; Gaps 1;

QY 1 MAACRSYKGLVAVITGGASGLATAPRLVGGASAVLLDPSNGGEAOKKLGNNCF 60
 DB 1 MAACRSYKGLVAVITGGASGLATAPRLVGGASAVLLDPSNGGEAOKKLGNNCF 60
 QY 61 APADVTSEKDVOTALAKGKFGKRVAVNACAGIAVASKTYNLKGGTHLEDFQRYLDV 120
 DB 61 APADVTSEKDVOTALAKGKFGKRVAVNACAGIAVASKTYNLKGGTHLEDFQRYLDV 120
 QY 121 NLMGTFNIVRLVAGMGONPEPDGQGRVINTASVAAPFEGVGOAAVSAKSGIVGML 180
 DB 121 NLMGTFNIVRLVAGMGONPEPDGQGRVINTASVAAPFEGVGOAAVSAKSGIVGML 180
 QY 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKVFANFLASQVPPSRLDGPAEYAHVQAI 240
 DB 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKVFANFLASQVPPSRLDGPAEYAHVQAI 240
 QY 241 IENPFLNGEVIRLDGAIKMP 261
 DB 241 IENPFLNGEVIRLDGAIKMP 261
 QY 232 IENPFLNGEVIRLDGAIKMP 252

RESULT 2

Q99N15 PRELIMINARY; PRT; 261 AA.
 AC Q99N15;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
 DE Short chain L-3-hydroxycyl-CoA dehydrogenase.
 GN HSD17B10 OR SCHAD.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21096701; PubMed=11165016;
 RA He X.Y., Merz G., Chu C.H., Lin D., Yang Y.Z., Mehta P., Schulz H.,
 RA Yang S.Y.;
 RA "Molecular cloning, modeling, and localization of rat type 10 17beta-
 RT hydroxysteroid dehydrogenase.";
 RL Mol. Cell. Endocrinol. 171:89-98(2001).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
 CC EMBL; AF233685; AA015008.1; -;
 DR HSDP; 070351; 1E6W.
 DR MGD; MG1:133871; Hsd17b10.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KM Oxidoreductase.
 SQ SEQUENCE 261 AA; 27273 MW; F371ED8A15CEEFNF CRC64;

Query Match

Best Local Similarity 89.9%; Score 1159; DB 11; Length 261;
 Matches 229; Conservative 18; Mismatches 14; Indels 0; Gaps 0;

QY 1 MAACRSYKGLVAVITGGASGLATAPRLVGGASAVLLDPSNGGEAOKKLGNNCF 60
 DB 1 MAACRSYKGLVAVITGGASGLATAPRLVGGASAVLLDPSNGGEAOKKLGNNCF 60
 QY 61 APADVTSEKDVOTALAKGKFGKRVAVNACAGIAVASKTYNLKGGTHLEDFQRYLDV 120
 DB 61 APADVTSEKDVOTALAKGKFGKRVAVNACAGIAVASKTYNLKGGTHLEDFQRYLDV 120
 QY 121 NLMGTFNIVRLVAGMGONPEPDGQGRVINTASVAAPFEGVGOAAVSAKSGIVGML 180
 DB 121 NLMGTFNIVRLVAGMGONPEPDGQGRVINTASVAAPFEGVGOAAVSAKSGIVGML 180
 QY 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKVFANFLASQVPPSRLDGPAEYAHVQAI 240
 DB 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKVFANFLASQVPPSRLDGPAEYAHVQAI 240
 QY 241 IENPFLNGEVIRLDGAIKMP 261
 DB 241 IENPFLNGEVIRLDGAIKMP 261

RESULT 3

Q9CYT3 PRELIMINARY; PRT; 261 AA.
 AC Q9CYT3;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
 DE Hydroxycyl-coenzyme A dehydrogenase, type II.
 GN HSD17B10 OR HADH2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai T., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Thu Jun 26 06:55:05 2003

us-09-931-186-20.rspt

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:22:37 ; Search time 31.6667 Seconds
(without alignments)
1698.262 Million cell updates/sec

Title: US-09-931-186-20
Perfect score: 1304
Sequence: 1 MAACRSYKGLVAVITGAS.....ENPLNGEVITLDGAIKMP 261

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database: SPRENBL_21:
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.todent:*
12: sp.virus:*
13: sp.unclassified:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1241.5	95.2	252	4	Q96HD5
2	1159	88.9	261	11	Q99N15
3	1155	88.6	261	11	Q9CYT3
4	984	75.5	196	4	Q8TCV9
5	750	57.5	258	5	Q19102
6	722	55.4	255	16	Q910T0
7	713	54.7	255	16	Q8IBS0
8	691.5	53.0	252	16	Q8XWEO
9	673.5	51.6	250	16	Q06544
10	672	51.5	255	16	Q92YS1
11	669	51.3	253	16	Q98BM4
12	654	50.2	255	2	Q9AHY1
13	644	49.4	257	16	Q8UR12
14	609	46.7	126	11	Q9DCX5
15	603.5	46.3	264	5	Q8T2L7
16	597	45.8	260	16	Q9ABU6

17	386	29.6	443	2	Q935J3	Q935J3 myxococcus
18	375.5	28.8	246	16	Q8XJH1	Q8XJH1 clostridium
19	357.5	27.4	244	16	Q931D6	Q931D6 streptococ
20	355	27.2	252	16	Q9HW15	Q9HW15 pseudomonas
21	345.5	26.5	249	16	Q97DA6	Q97DA6 clostridium
22	339.5	26.0	247	16	Q8R9W0	Q8R9W0 thermomater
23	335.5	25.7	246	16	Q9KA03	Q9KA03 bacillus ha
24	335.5	25.7	297	3	Q42774	Q42774 neurospora
25	334.5	25.7	251	16	Q8YWT0	Q8YWT0 anabaena sp
26	332	25.2	246	16	Q9K36	Q9K36 bacillus ha
27	328.5	25.2	248	2	Q9K1E1	Q9K1E1 thauera aro
28	328.5	25.2	260	16	Q8B068	Q8B068 streptococ
29	327.5	25.1	243	16	Q9FBC3	Q9FBC3 streptococ
30	326.5	25.0	243	16	Q9CHF7	Q9CHF7 lactococcus
31	325	24.9	262	2	Q9L9F8	Q9L9F8 streptococ
32	324.5	24.9	260	4	Q96KX9	Q96KX9 homo sapien
33	323	24.8	271	10	Q94G09	Q94G09 cucumis sat
34	322	24.7	261	13	Q8U0M4	Q8U0M4 cryzias lat
35	321	24.6	263	16	Q9KYM4	Q9KYM4 streptococ
36	320.5	24.6	246	2	Q9EX74	Q9EX74 rhodococcus
37	320	24.5	271	10	Q94G10	Q94G10 cucumis sat
38	319.5	24.5	261	6	Q8WMA4	Q8WMA4 macaca mula
39	319	24.5	258	2	Q9F8V0	Q9F8V0 streptococ
40	317	24.3	299	17	Q97UK6	Q97UK6 sulfolobus
41	316.5	24.3	259	16	Q8U616	Q8U616 agrobacteri
42	316.5	24.3	313	2	Q93HC0	Q93HC0 streptococ
43	315.5	24.2	296	16	Q9ABX6	Q9ABX6 cauliobacter
44	313.5	24.0	240	17	Q9UY54	Q9UY54 pyrococcus
45	313.5	24.0	249	2	Q9A7J2	Q9A7J2 thauera aro
46	313	24.0	247	16	Q9PFF6	Q9PFF6 xylella fas
47	313	23.9	262	16	Q8IDB4	Q8IDB4 bruceella me
48	312	23.9	237	4	Q8WT8	Q8WT8 homo sapien
49	311.5	23.9	244	16	Q8ZFF5	Q8ZFF5 yeastina pe
50	310.5	23.8	260	17	Q8UB33	Q8UB33 pyrococcus
51	310	23.8	256	16	Q8ZB06	Q8ZB06 yeastina pe
52	310	23.8	267	10	P93697	P93697 vigna ungu
53	309	23.7	253	16	Q8U759	Q8U759 agrobacteri
54	305.5	23.7	247	16	Q8Y6D0	Q8Y6D0 listeria mo
55	304	23.4	273	2	Q9F5J1	Q9F5J1 streptococ
56	303.5	23.3	236	11	Q91VT4	Q91VT4 mus musculu
57	303.5	23.3	247	16	Q92AK1	Q92AK1 listeria in
58	303	23.2	248	2	Q9ZFF9	Q9ZFF9 bacillus me
59	303	23.2	248	16	Q8U9B5	Q8U9B5 agrobacteri
60	302.5	23.2	249	2	Q9ABG5	Q9ABG5 geobacillus
61	302.5	23.2	263	2	Q955F7	Q955F7 streptococ
62	300.5	23.0	258	16	Q93339	Q93339 mycobacteri
63	300.5	23.0	296	5	Q9XX28	Q9XX28 caenorhabdi
64	300	23.0	250	2	Q56840	Q56840 xanthobacte
65	300	22.9	252	17	Q97UA4	Q97UA4 sulfolobus
66	298	22.9	255	17	Q9H041	Q9H041 halobacteri
67	298	22.9	260	16	Q9FBN1	Q9FBN1 streptococ
68	297.5	22.8	254	16	Q92P88	Q92P88 rhizobium m
69	297.5	22.8	267	2	Q9L8G2	Q9L8G2 leifsonia a
70	297.5	22.8	538	2	Q8YV75	Q8YV75 rhizobium s
71	297	22.8	265	16	Q9S2E4	Q9S2E4 streptococ
72	296	22.7	245	16	Q8YDN1	Q8YDN1 bruceella me
73	294.5	22.6	270	4	Q9URK3	Q9URK3 homo sapien
74	294	22.5	315	10	Q949M3	Q949M3 brassica na
75	294	22.5	320	10	Q93X62	Q93X62 brassica na
76	293.5	22.5	270	4	Q9EPX1	Q9EPX1 homo sapien
77	293	22.5	255	16	Q8RDG3	Q8RDG3 thermomater
78	293	22.5	258	16	Q93015	Q93015 rhizobium m
79	293	22.5	328	10	Q93X67	Q93X67 brassica na
80	293	22.5	246	2	Q93HB3	Q93HB3 streptococ
81	292	22.4	272	16	Q8YHE0	Q8YHE0 bruceella me
82	291.5	22.4	405	16	Q9B850	Q9B850 rhizobium l
83	289.5	22.2	254	10	Q949M2	Q949M2 brassica na
84	289.5	22.2	303	10	Q9SCU0	Q9SCU0 arabidopsis
85	288.5	22.1	244	16	Q8X815	Q8X815 escherichia
86	288.5	22.1	245	16	Q8RDH9	Q8RDH9 thermomater
87	288	22.1	243	16	Q8RG25	Q8RG25 fusobacteri
88	287.5	22.0	247	2	Q930F0	Q930F0 azotobacter
89	287.5	22.0	254	16	Q9RT26	Q9RT26 deinococcus

PT producing levodione reductase for converting levodione to actinol,
PT which is a useful chiral building block of naturally occurring
PT optically active compounds -

XX Claim 3; Page 15-16; 19pp; English.

XX This sequence shows levodione reductase. Levodione reductase has a
CC relative molecular mass of 142-155kD +/- 10kD consisting of four
CC homologous subunits each having a molecular mass of 36kD +/- 5kD. This
CC enzyme converts levodione to (4R,6R)-4-hydroxy-2,2,6-trimethyl-
CC cyclohexanone (actinol), which is a useful chiral building block of
CC naturally occurring optically active compounds such as zeaxanthin.

XX Sequence 267 AA:

Query Match 22.8%; Score 297.5; DB 22; Length 267;
Best Local Similarity 32.2%; Pred. No. 9,4e-21;
Matches 85; Conservative 45; Mismatches 97; Indels 37; Gaps 9;

QY 12 VAVITGASGLGATAEERLVGASAVLLDIPNSGGEAOKKLGNNCYFAP----ADVT 66
DB 15 VVLTGGGGGLGRATAVAFLAAGAKLSVDVSSGLEASKAAVLETAPDAEVLTVADVS 74
QY 67 SEKDVOIALAKGKFGRYDAVANCAGIAVASKTYNKKGQTHLEDFORVLDVNLGTF 126
DB 75 DEAOVEAYVTATTEFRGRIDGFEFNNAGIEGKQ----NPTEFTAEFDKYSINLRGVF 129
QY 127 ---NVIRLVAGEMQNEPDGGQGRVLIINTASVAFEGVGQAAYSASKGIYGMTLPI 182
DB 130 LGLEVLKIMR-----EGGS--GMVYNTASVGIRIGINQSGYAIAKHGVGLTRNS 179
QY 183 ADLAPIGIRVNTAPLGLFTPLTSL-----PEKVA-NFLASQVPPPSRLGDPPEY 233
DB 180 AVEYGRYGRINAIAPAIWTFPMVENSMMKOLDPENPRKAAEEFI--QVNPSSRYGEAPEI 237
QY 234 AHLVQALLEN--PELNGEVIRLDG 255
DB 238 AAVVAFLLSDDASIVNATVVPIDG 261

Search completed: June 23, 2003, 14:28:33
Job time : 41.6667 secs

disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. In addition, (1) affects biorhythms or circadian cycles of rhythms, fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAU28020-AAU28395 represent novel human secreted protein amino acid sequences of the invention.

Sequence 288 AA:

Query Match 23.0%; Score 300.5; DB 22; Length 288;
Best Local Similarity 31.5%; Pred. No. 5.3e-21;
Matches 86; Conservative 44; Mismatches 116; Indels 27; Gaps 7;

1 MAACRSYKGLVAVITGASGLGLTAERLVGQASAVLLDLPNSGGEAQAQKLGNNCFV 60
10 MATGR-YAKKAVYTGSGRGAGIVAFVNSGARVYICDDESGRGLDELPGLI 68
61 AADVTSEKVOATALAKKRGVDVAVNCAGIVASKTYLKKGQTHLEDFORVLDV 120
69 SCQDVYQEDDVKTIVSETIRFRGRDCCVNNAGHPP-ORPEETSAHGFRQLEL 123
121 NLMGFENVIRLVAGEGQNEPDGQGRVYIINTASVAFAEGQVGAASASKSGIVGTL 180
124 NLGTTTLTKLALPYLRKQ-----GNVNISSLVGALGQACAVPYATGAVTAMTK 176
181 PIARDLAPGIRVMTAPLFGTPLTSL-PEKVA-NFLAS-----QVFPSPRL 227
177 AALDESPYGVAVNCISPCINMTPLMEELALMPRPATIRBGLAAGRSQVQIOPLRM 236
228 GDPAEY-AHLVQALIIENPLNGEVIRLDGAIIM 259
237 GDPAEVGAANVFLASBANFCTGIXLLVYGAEI 269

RESULT 24
ABP39667
ID ABP39667 standard; Protein: 263 AA.

AC ABP39667;

DT 24-JUL-2002 (first entry)

Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4512.

Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
antibacterial; gene therapy.

Staphylococcus epidermidis.

US6380370-B1.

30-APR-2002.

13-AUG-1998; 98US-0134001.

14-AUG-1997; 97US-055779P.

08-NOV-1997; 97US-064964P.

(GENO-) GENOME THERAPEUTICS CORP.

Doucette-Stamm LA, Bush D;

WPI, 2002-381255/41.

N-PSDB; ABN92212.

Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections -

PS Disclosure; SEQ ID 4512; 267pp; English.

ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP3124 to ABP3960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.
N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site.

Sequence 263 AA:

Query Match 22.9%; Score 298; DB 23; Length 263;
Best Local Similarity 32.3%; Pred. No. 8.2e-21;
Matches 85; Conservative 43; Mismatches 107; Indels 28; Gaps 6;

12 VAVITGASGLGLTAERLVGQASAVLLDLPNSGGEAQAQKLGNNCFV 68
11 VAVITGAAGIGLKIARLEFDGSLVDFENAVAKESKESKEQENAVAKADVSNR 70
69 KDVOATALAKKRGVDVAVNCAGIVASKTYLKKGQTHLEDFORVLDVLMGFENV 128
71 DVQSVLNVQVVEHGDNLVNNAGLGPMTPI-----ESVTEQEFNVGVVGVFWG 124
129 IRLVAGMGQNEPDGQGRVYIINTASVAFAEGQVGAASASKSGIVGTLPIARDLAP 188
125 IQAAIEQF-----DKLHGKILNATQAGVEGNAGLSLSTFVAVRGLTVAAARDLAE 179
189 IGRVMTAPLFGTPLTSLPEKVA-NFLASQVFPSPRLDPAEVANLV 237
180 KNIVVNAFAPGIVETPMKKGIAXELABENNQPMWGWKQFTDIAL-KRLSKEDVAVNV 238
238 QAIL-ENPFLNGEVIRLDGAIIR 258
239 SFLAGSDSYITGQTITVDGMR 261

RESULT 25
AAB47459
ID AAB47459 standard; Protein: 267 AA.

AC AAB47459;

DT 13-DEC-2001 (first entry)

Levodione reductase.

Levodione reductase; homologous subunit; levodione; primer; amplify; (4R,6R)-4-hydroxy-2,2,6-trimethylcyclohexanone; actinol; zeaxanthin;

PCR; polymerase chain reaction.

Corynebacterium aquaticum.

EP1122315-A1.

08-AUG-2001.

29-JAN-2001; 2001EP-0101940.

01-FEB-2000; 2000EP-0101665.

(HOFF) HOFFMANN LA ROCHE & CO AG F.

Shimizu S, Wada M;

WPI, 2001-551347/62.

N-PSDB; AAB43285.

New Corynebacterium aquaticum levodione reductase gene, useful for

XX 25-OCT-2000 (first entry)
 DT XX
 DE Bacillus megaterium 3-keto-acyl-CoA reductase Phab.
 XX
 KW Polyhydroxyalkanoate; polyhydroxybutyrate; transgenic plant; Phab;
 KW 3-keto-acyl-CoA reductase.
 XX
 OS Bacillus megaterium.
 XX
 PN WO200040730-A1.
 PD 13-JUL-2000.
 XX
 PF 07-JAN-2000; 2000WO-US00364.
 XX
 PR 07-JAN-1999; 99US-0115592.
 XX
 PA (UYMA-) UNIV MASSACHUSETTS.
 XX
 PI Cannon MC, Cannon FC, McCoool GJ, Valentin HE, Gruys KJ;
 XX
 DR WPI: 2000-532624/48.
 DR N-PSDB: AAA50142.
 XX
 PT New nucleic acid fragment encoding proteins involved in
 PT polyhydroxyalkanoate (PHA) biosynthesis, useful in the production of
 PT transgenic plants or recombinant plant cells which can express PHAs
 PT such as polyhydroxybutyrate.
 XX
 PS Claim 85; Page 137-138; 153pp; English.
 XX
 CC The present sequence is that of Phab, a 3-keto-acyl-CoA-reductase
 CC protein of Bacillus megaterium. The sequence was deduced from an
 CC open reading frame identified in an isolated 7,916 bp fragment of
 CC B. megaterium strain 11561 genomic DNA (see AAA50142). The 7,916 bp
 CC DNA fragment includes genes encoding proteins (see AA95743-47)
 CC involved in polyhydroxyalkanoate (PHA) biosynthesis. Nucleic acids
 CC encoding these proteins are useful for creating transgenic plants or
 CC recombinant host cells which have the capability of expressing PHAs
 CC such as polyhydroxybutyrate, polyhydroxyvalerate,
 CC polyhydroxyhexanoate, polyhydroxyoctanoate, polyhydroxydecanoate or
 CC their copolymers. Claimed methods for preparing a PHA involve
 CC obtaining a plant or a cell comprising a nucleic acid encoding
 CC a 3-keto-acyl-CoA reductase (especially the present sequence), and
 CC a nucleic acid encoding a PHA synthase (see AA95747), and growing
 CC the plant or cell under conditions suitable for PHA production.
 CC
 XX
 SQ Sequence 247 AA:

Query Match 23.2%; Score 303; DB 21; Length 247;
 Best Local Similarity 29.1%; Pred. No. 2,4e-21;
 Matches 78; Conservative 59; Mismatches 93; Indels 38; Gaps 9;
 QY 7 SVKGLVAVITGASGIGLATAEKLYGCG-----ASAVILDPNGGGEQAOK 53
 DB 3 TQGGKVAIVYGGGKGAITRELASNGKVVAVNNSKESKAIVKEIKDNGGE---- 58
 QY 54 LGNCFVAPADVSEEDVOTALALAKGKGRVAVNACAGIAVASKTYMLKRGOTHTLE 112
 DB 59 -----IAYGADSVYVQAKHLEIFETKAFCQDILVNNNGI---TRDRFFKLGE----E 106
 QY 113 DFOGVLDVNLGTFENIRILVAGMGONEDDGGQGVITNTASVAEFQVQQAASAK 172
 DB 107 DMKKVDVNLHSYNTTSALTLHLESE---GGR---VINISIIQQAQGFQNTNSAK 160
 QY 173 GGIVGTLPIARDLAFIGIRVNTIARGLFGTPLLTSLEPKVANFELASQVPPSRIGDPAE 232
 DB 161 AGMLGFTKSLALELAKATGVYVNAICGFIETENYMAIPEDVAKIYAKIP-TRRLCHABE 219
 QY 233 YAH-LVQAITENFELNGEVIIRLDGAIRM 259
 DB 220 IARGVYTLAKDGAVITGOOLININGILYM 247

RESULT 23
 AAU28296
 ID AAU28296 standard; Protein: 288 AA.
 XX
 AC AAU28296;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secretory protein, Seq ID No 653.
 XX
 KW Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
 KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;
 KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 KW fertility; analgesic; pain; antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200166659-A2.
 PD 13-SEP-2001.
 XX
 PF 05-MAR-2001; 2001WO-US04942.
 XX
 PR 07-MAR-2000; 2000US-0519705.
 PR 19-MAY-2000; 2000US-0574454.
 PR 17-JUN-2000; 2000US-0596193.
 PR 14-JUL-2000; 2000US-0616847.
 PR 19-SEP-2000; 2000US-0665363.
 PR 20-OCT-2000; 2000US-0693267.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Xu C, Wehman T, Ren F, Ma Y, Zhou P;
 PI Zhao Qa, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
 XX
 DR WPI: 2001-589334/66.
 DR N-PSDB: AAS45196.
 XX
 PT Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders.
 XX
 PS Example 2; SEQ ID No 653; 107pp; English.
 XX
 CC The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing haematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I), (II) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions,
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and

DR N-PSDB; AAA89187.
XX
PT New human oxidoreductase proteins useful for diagnosing, treating or
PT preventing proliferative, neurological, genetic, smooth muscle,
PT autoimmune or inflammatory disorders associated with abnormal
PT expression of oxidoreductase proteins
XX
PS Claim 1(a): Page 83; 95pp; English.
XX
CC The present sequence is that of human oxidoreductase OXR-3, as
CC deduced from a cDNA clone (see AAA89187) isolated from a lung tumour
CC cDNA library. The protein shows homology to Escherichia coli
CC 3-oxoacyl-(acyl)-carrier protein, and includes a short-chain
CC dehydrogenase signature. OXR-3 is expressed in nervous, reproductive,
CC cardiovascular and gastrointestinal tissue, and may be involved in
CC cell proliferation and inflammation. The invention provides OXR-1
CC to 8 polypeptides (see AAB19926-33) and polynucleotides (see
CC AAA89185-92). It also provides methods for using these polypeptides
CC and polynucleotides for diagnosing, treating or preventing disorders
CC associated with expression of OXR, especially cell proliferative,
CC neurological, genetic, smooth muscle, and autoimmune/inflammatory
CC disorders. The proteins can also be used to screen for agonists
CC and antagonists useful for treating these conditions, while
CC antibodies that bind to OXR may be used for diagnosis or in assays
CC to monitor patient treatment.
XX
SQ Sequence 237 AA;
XX
Query Match 23.9%; Score 312; DB 22; Length 237;
Best Local Similarity 31.6%; Pred. No. 3.1e-22;
Matches 80; Conservative 42; Mismatches 105; Indels 26; Gaps 5;
XX
QY 12 VAVITGAGAGLGIATRIYVGGASAVLIDLPNSGGEQAATLGNVCYFAPADVTSEKV 71
DB 4 VCAVFGSGSGIRNAVQALMARGYRLAVARNLEGAAGAAGLGGDHAFSCDVAKEHDV 63
QY 72 QVALAKGKFGFVADVAVNCAGI-----AVASKTYNLKKGQHTDEDFQVRADVLMGTG 126
DB 64 QNTFEMEKLHGRVNLVNAAGINDGLLYRTK-----EDWVSCILHMLDSM 112
QY 127 NVIRLVAGMGONEDPGGQGVIIINTASVAAFEGOVQAAVSASKGIVGKTLPIARDL 186
DB 113 LTKKAMRTMIDQ-----QGGSIVVGSIVGLKGNSSQSVYASAKGGLVGFPSRLAKEV 166
QY 187 APIGIRVMTIAPGLGEGTPLLTLSPKRVANFLASQVFPFSLGDPKRVYHIVQATLENRL 246
DB 167 ARKIKVNVAVAPGFVHTDITKDLKEE--HKKNIPL-GRGQETLEVAAHVAVFLESPYI 222
QY 247 NSEVIRLDGAIRM 259
DB 223 TGHVLVVDGGLQ 235
XX
RESULT 21
ID ABB48892 standard; Protein; 247 AA.
XX
AC ABB48892;
XX
DE 05-FEB-2002 (first entry)
XX
XX Listeria monocytogenes protein #1596.
XX
XX Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
XX vitamin B12; bacterial infection; disease.
XX
XX Listeria monocytogenes.
XX
PN WO200177335-A2.
XX
XX 18-OCT-2001.
XX
XX 11-APR-2001; 2001WO-FR01118.

XX
PR 11-APR-2000; 2000FR-0004629.
XX
PA (INSP) INST PASTER.
XX
PI Buchrieser C, Frangoul L, Couve E, Rusnlok C, Eshti H, Dehoux P,
PI Dussurget O, Chetouani F, Nedjati H, Glaser P, Kunst F, Cossart P,
PI Daniels J, Goebel W, Kieft U, Kuhn M, Ng E, Vazquez-Boland JA,
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A,
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L,
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N,
PI Madueno E, De Paulos B, Wehlend J, Kaerst U, Entlian K, Hauf J,
PI Rose M, Voss H;
XX
XX WPI: 2002-010914/01.
XX
XX Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
XX and prevention of Listeria and related bacterial infections, and
XX related polypeptides
XX
XX Claim 6; SEQ ID No 1597; 192pp; French.
XX
XX The present invention relates to the genome sequence of Listeria
XX monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
XX it are useful for selecting probes and primers for detecting genes in L.
XX monocytogenes and related organisms, and for studying genetic
XX polymorphisms and other genomes. The present sequence is a protein
XX encoded from the genome sequence of the present invention. Proteins
XX expressed from the genome sequence are useful for raising specific
XX antibodies, identification of L. monocytogenes and related organisms, and
XX for biosynthesis and biodegradation, especially biosynthesis of Vitamin
XX B12. The genome sequence and proteins encoded by it are also useful for
XX selecting compounds that regulate gene expression and cell replication
XX and modulate L. monocytogenes-related diseases. In addition, the genome
XX sequence and proteins encoded by it are useful in pharmaceutical and
XX vaccines compositions for the treatment or prevention of infections by L.
XX monocytogenes and related organisms.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPD
XX at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 247 AA;
XX
Query Match 23.4%; Score 305.5; DB 23; Length 247;
Best Local Similarity 32.0%; Pred. No. 1.4e-21;
Matches 85; Conservative 45; Mismatches 103; Indels 33; Gaps 7;
XX
QY 7 SVKGLVAVITGAGAGLGIATRIYVGGASAVLIDLPNSGGEQA-----KTL-----GNNC 58
DB 2 TLQGVAVVVGSGSGIRDAINLAKGANIFF-----NYNGSPAEAEETKLVAEHGV 57
QY 59 VFAPADVTSEKDVQVATLAKGKFGVADVAVNCAGIVASKTNYLKGQHTLEDQVRV 118
DB 58 EAMKANVAIAEDVDVAFKQAIERGFVDILVNNAGITRDILNKRME-----DEMDVYI 111
QY 119 DVNIMCTFNVIIRLVAGMGONEDPGGQGVIIINTASVAAFEGOVQAAVSASKGIVG 178
DB 112 NINLKGTFCTKAVSRMMKQ-----RAKKIINMSVGLLIGNAGANVYAKAGVIGL 165
QY 179 TLPARDLAPIGITVMTIAPGLGEGTPLLTLSPKRVANFLASQVFPFSLGDPKRVYHIVQ 238
DB 166 TKTLARELAPRGIVNVAVAPGFVHTDITDITKDLKEKMAAQP-----IGAVGTEDIAN 221
QY 239 AII-----ENPFLNGEVIRLDGAIRM 259
DB 222 AVLFASDASKYITIGQTLISVDGGMV 247
XX
RESULT 22
ID AAY95746 standard; Protein; 247 AA.
XX
AC AAY95746;
XX

OS Pyrococcus abyssi.
XX FR2792651-A1.
XX 27-OCT-2000.
XX 21-APR-1999; 99FR-0005034.
XX 21-APR-1999; 99FR-0005034.
XX 21-APR-1999; 99FR-0005034.
XX (CNRS) CNRS CENT NAT RECH SCI.
XX (IFRE) IFREMER INST FR RECH EXPL MER.
XX Portier P, Thierry JC, Prieur D, Dietrich J, Lecompte O;
XX Querellou J, Weissenbach J, Saurin W, Heilig R;
XX WPI; 2001-126236/14.
XX New nucleotide sequences isolated from Pyrococcus abyssi encode
XX proteins useful in industry -
XX Claim 7; Pages 1087-1088; 1657pp; French.
XX
XX The present invention relates to the genomic sequence of Pyrococcus
XX abyssi (see AAF6431 and AAH4123-7) and P. abyssi proteins. P. abyssi is
XX a hyperthermophilic archaeon, which is isolated from deep-sea
XX hydrothermal vents. The present sequence is one such P. abyssi protein.
XX The proteins of the present invention have various potential industrial
XX uses, since the proteins are stable at very high temperatures, some up to
XX 110 degrees centigrade.
XX Note: This patent is in the same patent family as WO200065062, which
XX contains additional sequences as shown in AAB9132-AAB99143,
XX AAH5903-AAH5920 and AAG66436.
XX
XX Sequence 241 AA:
SQ
Query Match 24.0%; Score 313.5; DB 22; Length 241;
Best Local Similarity 35.3%; Pred. No. 2.2e-22;
Matches 91; Conservative 44; Mismatches 88; Indels 35; Gaps 8;
DB 8 VGLVAIVTGGASGLTATSLVQGSAYLLDLPNSGGEAQAQKILGNNC-----VF 60
DB 4 LKGRVALLTGSASRGIRALTEIAKRGVNVINRSN---BEAKKTEELCROQGVETLL 60
QY 61 APADVTSEKDVOTATLAKGKFGKRVDAVNCAGIAVASKTYNKKGGTHTEDEQRLVDY 120
DB 61 VKADVSNEEVEKEMKVIDKFRIDILINNAGI--LQKT---KPLEVTDEMDRVISV 115
QY 121 NLMTGFNYIRLVAGSEMGNEPDGQGVIIINTASVALEFGVQGAAYASASKGIVGWTL 180
DB 116 NLKGFVITQGEVLRN-----KKKIVNIAISIAKDGITVGPAAKGGIALTE 166
QY 161 PIARPLAIGIRVMTIAPGLTGLTLPILSLPERVANFLASQVFPFSLD---PPEYALV 237
DB 167 NLAIRHAP-NILVNVAAAGPVDTDLTSEMKEMLKTL-----SLTGDIAPSEVAAV 218
QY 238 QAIENPFLNGEVRIDG 255
DB 219 IFLLENDHITGEVIDVNG 236

KW (S)-4-halo-3-hydroxybutyric acid ester; 4-halo-acetoacetic acid ester;
KW beta-ketoacyl-acyl carrier protein reductase; acetoacetyl-CoA reductase;
KW polybeta-hydroxy fatty acid biosynthesis; optically active;
KW 4-halo-3-hydroxybutyric acid ester.
XX
XX Bacillus subtilis.
XX EP953375-A2.
XX 10-NOV-1999.
XX 10-MAY-1999; 99EP-0109403.
XX
XX 08-MAY-1998; 98P-0126507.
XX 21-OCT-1998; 98UP-0300178.
XX 05-APR-1999; 99JP-0098205.
XX
XX (DAIL) DAICEL CHEM IND LTD.
XX Yamamoto H;
XX WPI; 2000-118183/11.
XX N-PDB; AA245749.
XX
XX Producing optically pure (S)-4-halo-3-hydroxybutyric acid ester -
XX Claim 6; Page 19-20; 34pp; English.
XX
XX The present sequence represents a beta-ketoacyl-ACP reductase protein
XX of Bacillus subtilis. The beta-ketoacyl-ACP reductase enzyme constitutes
XX a type II fatty acid synthetase. The enzyme has an extremely high
XX reducing activity and stereoselectivity towards 4-chloroacetoacetic
XX acid ester. The specification describes a method for producing a
XX (S)-4-halo-3-hydroxybutyric acid ester. The method comprises
XX asymmetrically reducing 4-halo-acetoacetic acid ester or its
XX derivative with beta-ketoacyl-acyl carrier protein reductase
XX constituting type II fatty acid synthase, or acetoacetyl-CoA
XX reductase constituting the polybeta-hydroxy fatty acid biosynthesis
XX system. The novel method is used to produce optically active
XX 4-halo-3-hydroxybutyric acid ester, with a high purity.
XX
XX Sequence 248 AA:
SQ
Query Match 24.0%; Score 312.5; DB 21; Length 248;
Best Local Similarity 29.7%; Pred. No. 2.9e-22;
Matches 76; Conservative 55; Mismatches 100; Indels 25; Gaps 6;
DB 13 AVITGASGLTATSLVQGSAYLLDLPNSGGEAQA-----KILGNNCVRAPADV 65
DB 9 AIVTGAIRGIGRSIALALAKSGANV---VNSGNEAKNEVYDEIKSGRAIAVKADV 65
QY 66 TSEKDVOTATLAKGKFGKRVDAVNCAGIAVASKTYNKKGGTHTEDEQRLVDVLMGT 125
DB 66 SNEDVQNMKTELVSFTSIDILVNNAGTRDNLIRNKE-----DEMDVYINILKGV 119
QY 126 FNVIRLVAGSEMGNEPDGQGVIIINTASVALEFGVQGAAYASASKGIVGWTLP 185
DB 120 FNCKRAVTRQMKO-----RSGRIINVSIVSGNPGQANVAAKAGVIGTKSSAKE 173
QY 186 LAPIGIRVMTIAPGLTGLTLPILSLPERVANFLASQVFPFSLD---PPEYALV 243
DB 174 LASRNTVNAIAAGFISTDTKTLAKVDQDEMILQIPL-RRGEPEDVSVVTFPLASGA 232
QY 244 PFLNGEVRIDG 259
DB 233 RYMTGOTLHIDGGMV 248

RESULT 19
AAU28156 standard; Protein; 237 AA.
AAU28156
AAU28156
AAU28156

XX Hasselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GT;
PI Yamamoto RT, Xu HH;
XX WPI: 2001-611495/70.
DR N-PSDB: AAS53167.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
XX Example 3: Seq ID No 10921; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence : 245 AA;

Query Match 24.6%; Score 320.5; DB 22; Length 245;
Best Local Similarity 33.7%; Pred. No. 4.7e-23;
Matches 84; Conservative 38; Mismatches 108; Indels 19; Gaps 5;

QY 15 ITGASGIGLTAERLVGQGSANVLD---LPSGSGEPAQKRGNNCVAPADVTESEKD 70
DB 10 ITGSTRGIGKVAALAFKAGANIVNRSSEITPQROETE--FGVKGIGSGDISPDA 67
QY 71 VOTALAKKGRFGRVAVNMCAGIAVASKTYNLKKGTHTLEDFQRYLDVLMGTFWIR 130
DB 68 AGEMQATVDQSGTIDIVNNAGIT-----NDKLLMTMEDPNACIDIVLGTFMNQ 121
QY 131 LVAGMGONEDPDQGGQGVITNTASVAFEGQVQAAYSASKGGIVGNTLPADLPAPIG 190
DB 122 QAVKMMRO-----RSGRITINMASVSGIMNVQANVAAKAGVGTGKSVAREVAPRG 175
QY 191 IRVMTIAPGLFGTPELTLSPKRVANFLASQVFPESRLDPAEYHIVLVAIIENFELNGEV 250
DB 176 ITCAALAGCFIOTETMTDVLSKRVKQMAQPILOT-FQGVEDVATAATFLAKSYITIGOV 234
QY 251 IRLDGAIRM 259
DB 235 VAVDGLVW 243

RESULT 15
AA028344
ID AA028344 standard; Protein: 257 AA.

AA028344;

18-DEC-2001 (first entry)

Novel human secretory protein, Seq ID No 701.

Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
ischemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
myotropic lateral sclerosis; platelet disorder; thrombocytopenia;

KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
KW gut protection; lung; liver fibrosis; immune deficiency; infection;
KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
KW fertility; analgesic; pain; antigen.

Homo sapiens.

MO200166689-A2.

13-SEP-2001.

05-MAR-2001; 2001WO-US04942.

07-MAR-2000; 2000US-0519705.

19-MAY-2000; 2000US-0574454.

17-JUN-2000; 2000US-0596193.

14-JUL-2000; 2000US-0616847.

19-SEP-2000; 2000US-0665363.

20-OCT-2000; 2000US-0693267.

WPI: 2001-589934/66.

N-PSDB: AAS45244.

Novel polypeptides and nucleic acids obtained from cDNA libraries
prepared from various human tissues, for diagnosis and treatment of
cancer, neurological, inflammatory, and autoimmune disorders -

Example 2: SEQ ID No 701; 107pp; English.

The invention relates to novel isolated human secreted polypeptides (I)
and polynucleotides (II). (I) and (II) are useful for treating
inflammatory conditions such as arthritis, nephritis, Crohn's disease,
ischemia-reperfusion injury, shock, sepsis, immune responses, and is
involved in increasing hematopoiesis, stem cell survival, bone growth
and remodeling. (I), (II) and modulators of (II) are useful for
propylaxis or treatment of one or more cancers. (II) is also useful for
creating transgenic animals useful for studying the in vivo activities of
the polypeptide as well as for studying modulators of the polypeptides.
(I) induces the proliferation of neural cells and regeneration of nerve
and brain tissue and is useful for the treatment of central and
peripheral nervous system diseases and neuropathies, such as Alzheimer's,
Parkinson's disease, Huntington's disease, and amyotrophic lateral
sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
activity, regulation of haematopoiesis and is useful for creating myeloid
or lymphoid cell disorders, platelet disorders such as thrombocytopenia
and for regeneration of bone, cartilage, tendon, ligament and/or nerve
tissue growth, and in tissue repair, healing of burns, incisions,
ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
disorders, or periodontal disease. Furthermore, (I) is also useful for
gut protection or regeneration and treatment of lung or liver fibrosis,
reperfusion injury in various tissues, various immune deficiencies and
disorders including severe combined immunodeficiency (SCID), bacterial or
fungal infections, autoimmune disorders e.g. multiple sclerosis,
rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
reactions and conditions, such as asthma or other respiratory problems.
In addition, (I) affects biorhythms or circadian cycles of rhythms,
fertility, metabolism, catabolism, anabolism, storage or elimination of
dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
analgesic effects or other pain reducing effects, immunoglobulin like
activity and can act as an antigen in a vaccine composition to raise an
immune response. AA028020-AA028395 represent novel human secreted protein
amino acid sequences of the invention.

Sequence 257 AA;

Query Match 24.38; Score 317; DB 22; Length 257;
Best Local Similarity 31.5%; Pred. No. 1.1e-22;

CC acids are useful for detecting the presence of proteins essential for the
CC viability of a bacterial cell wall in samples such as cells, tissues,
CC biological fluids, blood, serum, nose, ear or throat swabs with ligands,
CC and for detecting corresponding target nucleic acid molecules with
CC complementary sequences. The nucleic acids are also useful for
CC determining whether a genomic nucleotide sequence of interest is
CC essential for viability of a bacterial cell or whether it resides within
CC an operon, by integrating an exogenous nucleotide sequence comprising a
CC portion of an open reading frame of the genomic sequence of interest
CC (comprising 200-500 base pairs) into the genomic sequence of interest
CC which confers a selectable phenotype to the cell, and determining cell
CC viability with a selection agent such as chloramphenicol. The nucleic
CC acids and proteins are also useful as vaccines and for treating bacterial
CC infections with gene therapy and antisense therapy. The nucleic acids
CC also enable identification of targets suitable for the treatment of
CC antibiotic resistant bacterial infections.

XX Sequence 243 AA:

Query Match 25.1%; Score 327.5; DB 22; Length 243;
Best Local Similarity 34.7%; Pred. No. 9.7e-24;
Matches 87; Conservative 37; Mismatches 104; Indels 23; Gaps 6;

YY 15 ITGASGSLGATAEELVGGASAVLLDLPNSGGE-----AQAKKLGNNCYFAPADYTS 68
DB 10 ITGSRGIGLAIKAFAGAGANTYL-----NSRGAISELLAEFNSYGIKVPYIGSDVSDF 65
YY 69 KDVGATALLANGKFGVDVAVNACIAVASTYNIKKGQTHLEDFOFVLDPVNTMGFTNV 128
DB 66 ADARMTIDQALAEISLVVLYNNAGI--TQDTLMK---TEADFEKVLKVNLTGAFNM 119
YY 129 IRLVAGEMGNPDGQGGGVYIINTASVAEFGVGOAASASGSGITGMPLPARDIAP 188
DB 120 TQSVL-----KPMKAREGALINMSVVGIMGNQANVASKAGLIGFTKSVAREVAS 173
YY 189 IGRVMTIAPGLFGTPLTSLPEKYANFLASQVPPSRIGDPAEYAHLVQAIINPFLNG 248
DB 174 RRIRVNVIAPKIESDMTALISDKIKETALQIPW-KEFGQAEQVADLTFLAQGDYLTG 232
YY 249 EYIRLDGAIKM 259
DB 233 QVVAIDGGISM 243

RESULT 13

ABBS4087
ID ABBS4087 standard; Protein; 243 AA.

XX ABB54087;

XX 16-MAY-2002 (first entry)

XX Lactococcus lactis protein dabgl.

XX Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.

XX Lactococcus lactis IL1403.

XX FR2807446-A1.

XX 12-OCT-2001.

XX 11-APR-2000; 2000FR-0004630.

XX 11-APR-2000; 2000FR-0004630.

XX (INRG) INRA INST NAT RECH AGRONOMIQUE.

XX Bolotine A, Sorokline A, Renault P, Ehrlich SD;

XX WPI; 2002-043418/06.

XX New nucleotide sequence useful in the identification of Lactococcus

PT

PT lactis and related species -
XX Claim 6; SEQ ID No 789; 2504pp; French.

XX The present invention is related to a Lactococcus lactis nucleotide
CC sequence (ABBS4087) and related proteins (ABBS3300-ABBS5621). The
CC nucleic acid sequence is useful in the detection and/or amplification of
CC nucleic acid sequence, particularly to identify Lactococcus lactis or
CC related species. The proteins of the invention are useful for the
CC biosynthesis or biodegradation of a composition of interest. The
CC invention helps research in lactic bacteria, particularly useful in the
CC production of yogurt and cheese.
CC Note: The sequence data for this patent is based on equivalent patent
CC WO200177334 (published 18-OCT-2001) which is available in electronic
CC format directly from WIPO at http://wipo.int/pub/published_pct_sequences.

XX Sequence 243 AA:

Query Match 25.0%; Score 326.5; DB 23; Length 243;
Best Local Similarity 31.7%; Pred. No. 1.2e-23;
Matches 82; Conservative 48; Mismatches 104; Indels 25; Gaps 6;

YY 8 VKGLVAVITGASGLGATAEELVGGASAVLLDLPNSGGEQAKL-----GNNGYF 60
DB 3 IKKNVFTVSTGIGKALQFAKGSNLT-----NGRSALSELLAEFRAYGVKANG 57
YY 61 APADVTSEKDVQATALLAKKFGVDVAVNACIAVASTYNIKKGQTHLEDFOFVLDPV 120
DB 58 ISGDISKSEDAKQVMAEITLGSVILVNNAGI--TRDLSIKMSE---EDFESVLKI 111
YY 121 NMGTEFVRLVAGEMGNPDGQGGGVYIINTASVAEFGVGOAASASGSGITGMPL 180
DB 112 NLGAEFMTQAVL-----KPMTRASGALINMSVVGIMGNQANVASKAGLIGLTK 165
YY 181 PIARDLAPIGRMTIAPGLFGTPLTSLPEKYANFLASQVPPSRIGDPAEYAHLVQAI 240
DB 166 SIAREVAVRVNNAVAPGFIESDMTEVLSDYKDKAMKGIPIW-KFQGMPEELATATQPL 224
YY 241 IENPFLNGEYIRLDGAIKM 259
DB 225 AEOEYMTGQVLTIDGVSVM 243

RESULT 14

AAU33328
ID AAU33328 standard; Protein; 245 AA.

XX AAU33328;

XX 14-FEB-2002 (first entry)

XX Enterococcus faecalis cellular proliferation protein #615.

XX Antisense; prokaryotic cellular proliferation protein;

XX antibiotic; antibacterial; drug design.

XX Enterococcus faecalis.

XX WO200170955-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US09180.

XX 21-MAR-2000; 2000US-191078P.

XX 23-MAY-2000; 2000US-206848P.

XX 26-MAY-2000; 2000US-207727P.

XX 23-OCT-2000; 2000US-242578P.

XX 27-NOV-2000; 2000US-253625P.

XX 22-DEC-2000; 2000US-257931P.

XX 16-FEB-2001; 2001US-269308P.

XX (ELIT-) ELITRA PHARM INC.

DB 66 ADARKMDQAIALGSDVLYNNAGI--TQDTLMKMK-----TEADFEKVLKVNLTGAFNM 119

QY 129 IRLVAGEMQNEPDGQGRVITINTASVAAFEGVQQAISAKSGIVGMTLPARDLAP 188

DB 120 TOSYL-----KPMKAREGAIINMSSVYGLMGNIGQANVYASAKGLIGFTKSVAREVAS 173

QY 189 IGRVMTIAPGLFGTPLTSLPEKVFANFLASOVPPSPRLGDPAEVYAHVQAIIENPFLNG 248

DB 174 RNRIVNYIAPGMIESDNTALISDKIKETLAQIIPM-KEFGQAEQVADLTIVFLAGODYLTG 232

QY 249 EVIRLDGAIRM 259

DB 233 QVIAIDGGLSM 243

RESULT 11

AAU37988

ID AAU37988 standard; Protein; 243 AA.

AC AAU37988;

XX 14-FEB-2002 (first entry)

DT 14-FEB-2002 (first entry)

DE Streptococcus pneumoniae cellular proliferation protein #417.

XX

KW Antisense; prokaryotic cellular proliferation protein;

KW antibiotic; antibacterial; drug design.

XX

OS Streptococcus pneumoniae.

XX

PN WO200170955-A2.

PD 27-SEP-2001.

XX

PF 21-MAR-2001; 2001WO-US09180.

XX

PR 21-MAR-2000; 2000US-191078P.

PR 23-MAY-2000; 2000US-206848P.

PR 26-MAY-2000; 2000US-207727P.

PR 23-OCT-2000; 2000US-242578P.

PR 27-NOV-2000; 2000US-253625P.

PR 22-DEC-2000; 2000US-257931P.

PR 16-FEB-2001; 2001US-269308P.

XX

PA (ELIT-) ELITRA PHARM INC.

PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

PI Yamamoto RT, Xu HH;

XX

DR N-PSDB; AAS55847.

XX

PT New polynucleotides for the identification and development of

PT antibiotics, comprise sequences of antisense nucleic acids -

XX

PS Example 3; Seq ID No 13581; 511pp; English.

XX

XX The invention relates to antisense inhibitors of genes essential to

CC prokaryotic cellular proliferation, their use in identifying the

CC genes, their use in the discovery of novel antibiotics, the essential

CC genes, themselves and the encoded proteins. The prokaryotes used are

CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella

CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The

CC invention is also useful for the identification of potential new targets

CC for antibiotic development. The antisense nucleic acids can also be used

CC to identify proteins used in proliferation, to express these proteins,

CC and to obtain antibodies capable of binding to the expressed proteins.

CC The proteins can be used to screen compounds in rational drug discovery

CC programmes. The antisense nucleic acid sequence is also useful to screen

CC for homologous nucleic acids which are required for cell proliferation in

CC a wide variety of organisms. The present sequence represents an

CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic

CC format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.

XX

XX Sequence 243 AA;

QY

DB 15 ITGASGSLGATLAEVLVGGASAVLIDLPNSGGE-----AQAKTIGNNCVAPADVYSE 68

DB 10 ITGSSRIGIATIAHKFAQAAGANTVL-----NSRGAISEELLAEFSNGIVVPISGVSDP 65

QY 69 KDYQTALALAKKFGKRGVAVNCAGTAVASKTYNLKKQGTHTLDEPQVLYDNLMGTFFV 128

DB 66 ADARKMDQAIALGSDVLYNNAGI--TQDTLMKMK-----TEADFEKVLKVNLTGAFNM 119

QY 129 IRLVAGEMQNEPDGQGRVITINTASVAAFEGVQQAISAKSGIVGMTLPARDLAP 188

DB 120 TOSYL-----KPMKAREGAIINMSSVYGLMGNIGQANVYASAKGLIGFTKSVAREVAS 173

QY 189 IGRVMTIAPGLFGTPLTSLPEKVFANFLASOVPPSPRLGDPAEVYAHVQAIIENPFLNG 248

DB 174 RNRIVNYIAPGMIESDNTALISDKIKETLAQIIPM-KEFGQAEQVADLTIVFLAGODYLTG 232

QY 249 EVIRLDGAIRM 259

DB 233 QVIAIDGGLSM 243

RESULT 12

AAU01032

ID AAU01032 standard; Protein; 243 AA.

AC AAU01032;

XX

DT 02-OCT-2001 (first entry)

DE CFE 35 protein sequence.

XX

KW Antibacterial; vaccine; gene therapy; bacterial cell wall viability;

KW CFE; CEG; Conserved Essential Gene; bacterial infection;

KW antisense therapy; antibiotic resistance.

XX

OS Streptococcus pneumoniae.

XX

PN WO200149721-A2.

PD 12-JUL-2001.

XX

PF 29-DEC-2000; 2000WO-US35604.

XX

PR 30-DEC-1999; 99US-0174089.

XX

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

PI Dougherty TJ, Pucci MJ, Dougherty BA, Davison DB, Brucoleri RE;

PI Thanassi JA;

XX

DR N-PSDB; AAH90731.

XX

PT Nucleic acids encoding conserved essential genes involved in bacterial

PT replication which are potential targets for the treatment of antibiotic

PT resistant bacterial infections -

XX

PS Claim 27; Page 273; 380pp; English.

XX

XX The present invention relates to nucleic acids (AAH90701-AAH90918)

CC encoding polypeptides (AAU01002-AAU01114), which are essential for the

CC viability of a bacterial cell wall. The acronym CFE stands for "CEG For

CC Expression", where CEG stands for "Conserved Essential Gene". The nucleic

OS Streptococcus pneumoniae.
XX XX
XX W0200044895-A1.
XX PN
XX 03-AUG-2000.
XX PD
XX 19-JAN-2000; 2000WO-US01131.
XX PR
XX 27-JAN-1999; 99US-0239052.
XX PR
XX (SMK) SMITHKLINE BEECHAM CORP.
PI Holmes DJ, Mooney J, Zhong YY, Debouck C, Jaworski DD, Wang M;
PI Warren RL, Kosmatka AL, McDevitt D, Ingraham KA, Chalker AF;
PI So CY, Wallis NG, Pearson SC;
XX
XX WPI: 2000-482971/42.
DR N-PSDB; AAA174684.
DR
PT FabG polypeptide, isolated from Streptococcus pneumoniae, is used to
PT treat microbial diseases, identify agonists and antagonists for
PT treating microbial infections and to detect diseases associated with
PT microbial infections -
XX
XX
PS Claim 1; Page 3; 40pp; English.
XX
XX The present sequence is a FabG (2-oxoacyl-acyl carrier protein
CC reductase) polypeptide. A full length FabG gene was isolated from a
CC Streptococcus pneumoniae 0100993 DNA library in E. coli. FabG
CC polynucleotides and polypeptides are used for detection and treatment of
CC microbial diseases. They may also be used to identify antagonists and
CC agonists which can then be used to treat microbial diseases. Compounds
CC that interfere with the initial physical interaction between a pathogen
CC and a host have been identified. The compounds are able to prevent the
CC adhesion of bacteria to mammalian extracellular proteins in wounds,
CC prevent adhesion between mammalian extracellular proteins and bacterial
CC FabG proteins which mediate tissue damage and/or to block normal
CC progression of pathogenesis in infections mediated by implantation of
CC in-dwelling devices or other surgical techniques. The FabG
CC polypeptides, polynucleotides, antagonists and agonists are especially
CC useful in the treatment of Helicobacter pylori infection. They may be
CC used to decrease H. pylori-induced cancers and to prevent, inhibit
CC and/or cure gastric ulcers and gastritis.
XX
XX
XX Sequence 243 AA;
SO
Query Match 25.2%; Score 328.5; DB 21; Length 243;
Best Local Similarity 35.1%; Pred. No. 7.7e-24;
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6
OY 15 ITGSGAGLGATVATFERYVGOGASAVLDDPNSGGE-----AQAKKLGNNCFAPADYSE 68
DB 10 ITSSSGIGLAIHAHKAAGAGANTIVL-----NSRGALSERLAEFNSYGIKVPISGVSDF 65
OY 69 KDVOALALAKGFGRHYDVAVNACAGIAVASTYNIKKGQHTLEDFOVLVDVNLMGTFNV 128
DB 66 ADARKMIDDAIELSGVDVLYNNAGI--TODTLMKM-----TEADFEKVLKVMLTAFNM 119
OY 129 IRIYAGBMGONEPDQGGRGVLIINFTASAEFGVGOGAAYASGGIVGTPLPIARDLAP 188
DB 120 TQSVL-----KMMKAREGALINNSSVYGLMNGNINQANTYASAKAGLIGTKVAAREVAS 173
OY 189 IGRVMTIAGLEFGTLLTSLPEKXANFLASQVPPPSLGDPPAYAHVVOAITENPPLNG 248
DB 174 RNRIVRVVIAAGMIESDMTALISDKIKETLQAIPIW-KEFGQAEQVADLVTFELGQDYLTIG 232
OY 249 EVIRLDGAIRM 259
DB 233 QVTAIDGGLSM 243

XX	AAU37767	standard; Protein; 243 AA.
AC	AAU37767;	
DT	14-FEB-2002	(first entry)
DE	Streptococcus pneumoniae cellular proliferation protein #196.	
XX	Antisense: prokaryotic cellular proliferation protein;	
KM	antibiotic; antibacterial; drug design.	
OS	Streptococcus pneumoniae.	
PN	W0200170955-A2.	
PD	27-SEP-2001.	
PE	21-MAR-2001; 2001MO-US09180.	
XX	21-MAR-2000; 2000US-191078P.	
PR	23-MAY-2000; 2000US-206848P.	
PR	26-MAY-2000; 2000US-207727P.	
PR	23-OCT-2000; 2000US-242578P.	
PR	27-NOV-2000; 2000US-253625P.	
PR	22-DEC-2000; 2000US-257931P.	
PR	16-FEB-2001; 2001US-269308P.	
PA	(ELIT-) ELITRA PHARM INC.	
PI	Hasselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;	
PI	Yamamoto RT, Xu HH;	
XX	WPI; 2001-611495/70.	
DR	N-PSDB; AAS55626.	
XX	New polynucleotides for the identification and development of	
PT	antibiotics, comprise sequences of antisense nucleic acids -	
XX		
PS	Example 3; Seq ID No 13360; 511pp; English.	
XX	The invention relates to antisense inhibitors of genes essential to	
CC	prokaryotic cellular proliferation, their use in identifying the	
CC	genes, their use in the discovery of novel antibiotics, the essential	
CC	genes themselves and the encoded proteins. The prokaryotes used are	
CC	Bacteriella coli, Staphylococcus aureus, Salmonella typhi, Klebsiella	
CC	pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The	
CC	invention is also useful for the identification of potential new targets	
CC	for antibiotic development. The antisense nucleic acids can also be used	
CC	to identify proteins used in proliferation, to express these proteins,	
CC	and to obtain antibodies capable of binding to the expressed proteins.	
CC	The proteins can be used to screen compounds in rational drug discovery	
CC	programmes. The antisense nucleic acid sequence is also useful to screen	
CC	for homologous nucleic acids which are required for cell proliferation in	
CC	a wide variety of organisms. The present sequence represents an	
CC	essential prokaryotic cellular proliferation protein.	
CC	Note: The sequence data for this patent did not form part	
CC	of the printed specification, but was obtained in electronic	
CC	format directly from WIPO at	
CC	ftp.wipo.int/pub/published_pct_sequences.	
XX		
SO	Sequence 243 AA;	
Query Match	25.2%; Score 328.5; DB 22; Length 243;	
Best Local Similarity	35.1%; Pred. No. 7.7e-24;	
Matches	88; Conservative 36; Mismatches 104; Indels 23; Gaps 6	
15	ITGASGLGATATERTLWGASAVLLDLPNSGCE-----AQAKKLGNVCFAFADVTSE 68	
Db	10 ITGSSRRIGLAIAHKKRAGANIVL-----NMSGALISEBLLEFSNYGIKVPISGDVSDF 65	
99	KDVQTALALAKKGFGKYDAVANCAGIATAASKTYLNKKQGTHTLEDPCGVLDVNLGMGFNV 128	

XX New Streptococcus protein for the treatment or prevention of infection
 PT or disease caused by Streptococcus bacteria, such as meningitis, and
 PT for detecting a compound that binds to the protein -

PS Claim 1: Page 3542; 4525pp; English.

CC The invention relates to a protein (ABP25413-ABP30695) from group B
 CC Streptococcus (SBS) (Streptococcus agalactiae) or group A Streptococcus (SAS)
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
 CC the specification. The proteins have antibacterial and anti-inflammatory
 CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a
 CC biological sample. (I) is used to determine whether a compound binds to
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins.

SO Sequence 243 AA:

Query Match 27.1%; Score 353; DB 23; Length 243;
 Best Local Similarity 35.4%; Pred. No. 3.1e-26;
 Matches 92; Conservative 42; Mismatches 100; Indels 26; Gaps 6;

QY 8 VKGLVAVITGASGLATAEERLVGASAVLLDIPNSGGEAQAARL-----GNNCVF 60
 DB 3 IKNNI-FITGSTRIGGLAMAHQFASLEANIVL-----NRSALISELVASTFDYGVTVT 56

QY 61 AAPDVTSKDVOTATLALAKGKGRVDVAVNCAGIAVASTYMLKKGQHTLEDFFORVLDV 120
 DB 57 ISCDVSEASEAKMVEALIESLSIDVIVNNAIGIT-----NDKMLTKTEEDFFRVLKI 110

QY 121 NLGVTNVIRLVAGEGONPEPOGGGVYIINTASVAPEFGVGQAASASKGIYGMTL 180
 DB 111 NLGAFNMNOSYL-----KPMKAKAGALINVS SVGLTGNIGQANVAASAKMIGFTK 164

QY 181 PIKDLAPGIRMTAPGLTGPPLTSLPEKYANFLASQVPPPSRLGPAEYANLVQAI 240
 DB 165 SVAREVAARNICVNAAPFIESDMGVLPKMQEQILSQIPM-KRIGAKQEVAAHLASFL 223

QY 241 IENPFLNGEYIRLDGAIRMQ 260
 DB 224 VEODYITGVYIADGGMWQ 243

RESULT 8
 AAM80670
 ID AAM80670 standard; Protein; 243 AA.

XX AAM80670:
 AC
 XX
 DT 24-DEC-1998 (first entry)
 XX
 DE 5. pneumoniae fatty acid biosynthesis protein.
 XX
 KM Streptococcus pneumoniae protein; recombinant; gene expression; DNA chip;
 KM virulence; antibody; infection; detection; treatment; hypothetical;
 KM cell wall biosynthetic; external target; minimal gene set protein.
 XX Streptococcus pneumoniae.
 OS
 XX
 PN WO9826072-A1.
 XX
 PD 18-JUN-1998.
 XX
 PF 09-DEC-1997; 97WO-US22578.

XX 13-DEC-1996; 96US-0036281.
 PR
 XX
 PA (EUIL) LILLY & CO ELL.

XX Baltz RH, Burgett SG, Dehoff BS, Hoskins JA, Jaskunas SR;
 PI Mills BJ, Norris FH, Peery RB, Hockey PK, Rostock PR;
 PI Skatard PJ, Smith MC, Solenberg PJ, Treadway PJ;
 PI Young Bellido ML;
 DR WPI: 1998-348529/30.

XX Streptococcus pneumoniae nucleic acid sequences - used in DNA chips
 PT for evaluating gene expression, and identification of virulence
 PT genes

PS Claim 3; Page 270; 333pp; English.

CC This sequence represents a S. pneumoniae fatty acid biosynthesis
 CC protein. The invention provides DNA sequences (AAM65201 to AAM65304)
 CC from the Streptococcus pneumoniae genome and corresponding protein
 CC sequences (AAM80605 to AAM80728). The protein sequences are classified as
 CC hypothetical, cell wall biosynthetic, external target, or minimal gene
 CC set proteins. A recombinant host containing a vector comprising any of
 CC the above nucleic acids can be used for the recombinant expression of the
 CC proteins. The invention also provides a DNA chip having arrayed on it at
 CC least 15 base pair fragment of any one or more of these DNA sequences.
 CC The DNA chip can be used methods for evaluating gene expression in S.
 CC pneumoniae and for identifying virulence genes in S. pneumoniae.
 CC Antibodies that selectively bind to the above proteins or peptide
 CC fragments can be used to treat S. pneumoniae infection. The antibodies
 CC can also be used to detect S. pneumoniae cells.

SO Sequence 243 AA:

Query Match 25.2%; Score 328.5; DB 19; Length 243;
 Best Local Similarity 35.1%; Pred. No. 7.7e-24;
 Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;

QY 15 ITGASGSLGATAEERLVGASAVLLDIPNSGGE-----AQAKKLNKCVFAPADVTSE 68
 DB 10 ITGSSRGIGLAIKAFNAAGANIVL-----NRSALISELVASTFDYGVTVT 56

QY 69 KDVOATLALAKGKGRVDVAVNCAGIAVASTYMLKKGQHTLEDFFORVLDVNLGTFNV 128
 DB 66 ADARKMIDQALAEIGSVIVLVNNAIGI-----TODTLMKMLK-----TEADFFRVLKI 119

QY 129 IRLVAGEGONPEPOGGGVYIINTASVAPEFGVGQAASASKGIYGMTLPIAPDLAP 188
 DB 120 TQSYL-----KPMKAKAGALINVS SVGLTGNIGQANVAASAKMIGFTK 173

QY 189 IGIRYMTAPGLTGPPLTSLPEKYANFLASQVPPPSRLGPAEYANLVQAIENPFLNG 248
 DB 174 RNIRVNVAPGMISDMATILSDRIKENTLAQIPM-KEFGAQEADVADLVFLAGODVLTG 232

QY 249 EVIRLDGAIRM 259
 DB 233 QYIADGGLSM 243

RESULT 9
 AAB15706
 ID AAB15706 standard; Protein; 243 AA.

XX AAB15706:
 AC
 XX
 DT 07-DEC-2000 (first entry)
 XX
 DE Streptococcus pneumoniae FabG polypeptide.
 XX
 KM Streptococcus pneumoniae; FabG; 3-oxoacyl-acyl carrier protein reductase;
 KM antibacterial; cytostatic; antitumor; cancer; gastric ulcer; gastritis;
 KM Helicobacter pylori infection; microbial infection.

Query Match 51.1%; Score 666.5; DB 18; Length 388;
 Best Local Similarity 53.5%; Pred. No. 1.5e-56;
 Matches 141; Conservative 35; Mismatches 69; Indels 9; Gaps 3;

QY 8 VKGLAVITGGASGLTAERLVGOGASAVLLDLPNSGGEAQAOKLGNMCVFAPADVTSE 67
 DB 143 IEGRFVVTGAASGASABRLAAGGAKVILADL-----AEPDAEGAVHAACDVTD 196
 QY 68 EKDVOITALAKGKRGVDVAVNCAGIVASKTYNLKKGQHTLEDFOFVLDVNLMTFN 127
 DB 197 ATAAQTALATADRFGRDLGVNCAGIAPAEEM--LGRDGHGIDSFARAVTINLIGSFN 254
 QY 128 VRLVAGEGONEPPOGGQGVIIINTASVAAFEGOVGOAAYSASKGIVGMLPIARDLA 187
 DB 255 MRLAEMAMARNEPVR-GERGVITNTASIAADGIGVAYTAASKAGVAGMTLPARDLA 313
 QY 188 PIGIRVMTIAPGLFETPLITSLPERVANFLASQVFPSPRLDDPAEYALVQAIIENPFLN 247
 DB 314 RGIIRVMTIAPGIFRTPLMELGPQDVODSLGAAYFPSPRLGEPSEYALLHHIILNPMLN 373
 QY 248 GEVIRLDGAIROMP 261
 DB 374 GEVIRLDGALRMAP 387

RESULT 6
 ABP28011
 ID ABP28011 standard; Protein: 244 AA.
 XX
 AC ABP28011;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Streptococcus polypeptide SEQ ID NO 5198.
 XX
 KM Streptococcus: GAS; group B streptococcus; Streptococcus agalactiae;
 KM group A streptococcus; Streptococcus pyogenes; antibacterial;
 KM antiinflammatory; infection; vaccine; meningitis; gene therapy.
 XX
 OS Streptococcus agalactiae.
 XX
 PN WO200234771-A2.
 XX
 PD 02-MAY-2002.
 XX
 PF 29-OCT-2001; 2001WO-GB04789.
 XX
 PR 27-OCT-2000; 2000GB-0026333.
 PR 24-NOV-2000; 2000GB-0028727.
 PR 07-MAR-2001; 2001GB-0005640.
 XX
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
 PI Tettelin H;
 XX
 DR WPI: 2002-352536/38.
 DR N-PSDB: ABN68642.
 XX
 PT New Streptococcus protein for the treatment or prevention of infection
 PT or disease caused by Streptococcus bacteria, such as meningitis, and
 PT for detecting a compound that binds to the protein -
 XX
 PS Claim 1: Page 3863; 4525pp; English.
 XX
 CC The invention relates to a protein (ABP25413-ABP30895) from group B
 CC Streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
 CC the specification. The proteins have antibacterial and antiinflammatory
 CC activity. (I), nucleic acids encoding (II), ABN6044-ABN71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for

the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a
 CC biological sample. (I) is used to determine whether a compound binds to
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins.

Sequence 244 AA;
 SQ

Query Match 27.9%; Score 363.5; DB 23; Length 244;
 Best Local Similarity 36.5%; Pred. No. 3e-27;
 Matches 92; Conservative 38; Mismatches 99; Indels 23; Gaps 5;

QY 15 ITGGASGLGATAERLVGOGASAVLLDLPNSGGE-----AQAOKLGNMCVFAPADVTSE 68
 DB 10 ITGSSRGIGLAIHQFQALGANIVL-----NGRSPISDDLAEFADYGVKVIATSGVSSP 65
 QY 69 KDVOITALAKGKRGVDVAVNCAGIVASKTYNLKKGQHTLEDFOFVLDVNLMTFN 128
 DB 66 EDANRMTKEATLASISGVAVLVNNAGIT-----NDKMLTKTYDEFSVLIKINLTGAFNM 119
 QY 129 IRLVAGEGONEPPOGGQGVIIINTASVAAFEGOVGOAAYSASKGIVGMLPIARDLA 188
 DB 120 TQSYL-----KPMTRAKOGAIIINISVGLTGVGQANVAASKAGIGFTKSVAREVA 173
 QY 189 IGIIRVMTIAPGLFETPLITSLPERVANFLASQVFPSPRLDDPAEYALVQAIIENPFLN 248
 DB 174 RGIIRVMTIAPGIFRTPLMELGPQDVODSLGAAYFPSPRLGEPSEYALLHHIILNPMLN 373
 QY 249 EVIRLDGAIROMQ 260
 DB 233 QVIALDGMQ 244

RESULT 7
 ABP27345
 ID ABP27345 standard; Protein: 243 AA.
 XX
 AC ABP27345;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Streptococcus polypeptide SEQ ID NO 3866.
 XX
 KM Streptococcus: GAS; group B streptococcus; Streptococcus agalactiae;
 KM group A streptococcus; Streptococcus pyogenes; antibacterial;
 KM antiinflammatory; infection; vaccine; meningitis; gene therapy.
 XX
 OS Streptococcus pyogenes.
 XX
 PN WO200234771-A2.
 XX
 PD 02-MAY-2002.
 XX
 PF 29-OCT-2001; 2001WO-GB04789.
 XX
 PR 27-OCT-2000; 2000GB-0026333.
 PR 24-NOV-2000; 2000GB-0028727.
 PR 07-MAR-2001; 2001GB-0005640.
 XX
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
 PI Tettelin H;
 XX
 DR WPI: 2002-352536/38.
 DR N-PSDB: ABN67976.
 XX

CC (see AAX00611 for described uses).
XX
SQ Sequence 227 AA;
Query Match 87.2%; Score 1137; DB 20; Length 227;
Best Local Similarity 99.6%; Pred. No. 8.1e-103;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 35 ASAYLLDLPNSGGEGQAARKLNCCVFAADYTSKDVQATALAKGKFGRYDVAVNCAGI 94
DB 1 ASAYLLDLPNSGGEGQAARKLNCCVFAADYTSKDVQATALAKGKFGRYDVAVNCAGI 60
QY 95 AVASTYTLKKGGQTHTLEDFOFVLDVNLMTGFNTIRLVAGMGQNEPDGQGRGVIINTA 154
DB 61 AVASTYTLKKGGQTHTLEDFOFVLDVNLMTGFNTIRLVAGMGQNEPDGQGRGVIINTA 120
QY 155 SVAAEEGGVGAAYASASKSGIVGMLTPIARDLAPIGIRVMTIAPGLFETPLISLPEKVA 214
DB 121 SVAAEEGGVGAAYASASKSGIVGMLTPIARDLAPIGIRVMTIAPGLFETPLISLPEKVC 180
QY 215 NFLASQVPEPSPRLGDPAEYAHVQAIENPFLNGEVIRLDGAIKMP 261
DB 161 NFLASQVPEPSPRLGDPAEYAHVQAIENPFLNGEVIRLDGAIKMP 227
RESULT 4
AAB62988
ID AAB62988 standard; Protein: 255 AA.
XX
AC AAB62988;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 15756.
XX
KM Drosophila: developmental biology; cell signalling; insecticide;
XX
KM pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
XX
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NX.
XX
PI Venter JC, Adams M, Li PWD, Myers EM;
XX
DR WPI; 2001-656860/75.
XX
DR N-PSDB; ABL07091.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX
PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX
PT interactions -
XX
PS Disclosure: SEQ ID NO 15756; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
XX
CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX
CC useful in developmental biology and in elucidating cell signalling and
XX
CC cell-cell interactions in higher eukaryotes for the development of
XX
CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX
CC discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded DNA
XX
CC sequences (ABB57731-ABB72072).
XX
CC (ABB57731-ABB72072).
XX
CC The sequence data for this patent did not form part of the printed
XX
CC specification, but was obtained in electronic format directly from WIPO
XX
CC at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 255 AA;
Query Match 69.8%; Score 910; DB 22; Length 255;
Best Local Similarity 68.9%; Pred. No. 1.4e-80;
Matches 175; Conservative 29; Mismatches 50; Indels 0; Gaps 0;
QY 8 VKGLVAVITGGASGLCLATAEPLVGGASAVLLDLPNSGGEGQAARKLNCCVFAADYTS 67
DB 2 IKNAVSLTVGGASGLCLATAEPLVGGASAVLLDLPNSGGEGQAARKLNCCVFAADYTS 61
QY 68 EKDVTALALANKFGFRVDVAVNCAGIAVASKTYLNRKQHTLEDFOFVLDVNLMTGFN 127
DB 62 EKDVSALCTAKKFGRLDVTVCAGTATVTFENKVAARLEDFQFVINITVGFEN 121
QY 128 VTRLVAGMGQNEPDGQGRGVIINTASVAAEEGGVGAAYASASKSGIVGMLTPIARDLA 187
DB 122 VTRLSAGLNGANEPDQGRGVIINTASVAAEDGQIGQAAYSKAAVGMILPIARDLS 181
QY 188 PIGIRVMTIAPGLFETPLISLPEKYANFLASQVPEPSPRLGDPAEYAHVQAIENPFLN 247
DB 182 TQGRICITAPGLFETPLISLPEKYANFLASQVPEPSPRLGDPAEYAHVQAIENPFLN 241
QY 248 GEVIRLDGAIKMP 261
DB 242 GEVIRLDGAIKMP 255
RESULT 5
AAW06513
ID AAW06513 standard; Protein: 388 AA.
XX
AC AAW06513;
XX
DT 08-MAR-1997 (first entry)
XX
DE Flavobacterium ORF-5 gene product.
XX
DE Flavobacterium ORF-5 gene product.
XX
KM Carotenoid; lycopene; beta-carotene; echinenone; cantaxanthin;
XX
KM zeaxanthin; adonixanthin; astaxanthin.
XX
OS Flavobacterium sp. R1534 WT (ATCC 21588).
XX
PN EP747483-A2.
XX
PN EP747483-A2.
XX
PD 11-DEC-1996.
XX
PF 29-MAY-1996; 96EP-0108556.
XX
PR 09-JUN-1995; 95EP-0108888.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Hohmann H, Pasamontes L, Tessier M, Van Loon A;
XX
DR WPI; 1997-023160/03.
XX
DR N-PSDB; AAT45143.
XX
PT Flavobacterium gene sequences encoding carotenoid biosynthesis
XX
PT enzymes - for the production of carotenoid(s), useful in foods and
XX
PT animal feeds
XX
PS Example 2; Fig 7; 80pp; English.
XX
CC A polypeptide (AAW06513) showing approx. 30% homology to
XX
CC streptomycete polyketide synthases was identified as the product
XX
CC of ORF-5 from a carotenoid gene cluster (see also AAT45143) of
XX
CC Flavobacterium sp. R1534. 5 Other open reading frames of the
XX
CC gene cluster coded for carotenoid biosynthetic enzymes (see also
XX
CC AAW06515-18 and AAW00871) and can be used to produce carotenoids in
XX
XX
SQ Sequence 388 AA;

Query Match	Best Local Similarity	87.9%: Score 1146; DB 21; Length 260;
Matches 226; Conservative 18; Mismatches 14; Indels 0; Gaps 0;		
QY 4 ACRSVKGLAVAVITGGASGLGATATERTLVGGQASAVLLDLPSNGSGEAQAKKLGANNCEVAPA 63		
Db 3 AVRSYKGLVAVAVITGGASGLGATATKRLVGQATAVLLDPVPSGEGAAQAKKLGESCIFAPA 62		
QY 64 DVTSEKDVQOTATLAKGKEGKGVADVAVNAGIAVASKTYNLTNRKGGTHTEDPQVTDVNM 123		
Db 63 NVTSEKELQAAALLTLAKKEFGRIIDVAVNAGIAVAKTYHQKKNKHTLEDQVYINVM 122		
QY 124 GTFNVIRLVAGEMGNEDPDGQGRVYIINTASVAAPFEGQVGAAYASASKGIVGTMPLPA 183		
Db 123 GTFNVIRLVAGEMGNEDPDGQGRVYIINTASVAAPFEGQVGAAYASASKGIVGTMPLPA 182		
QY 184 RDLAPIGIRVMTIAPGLFGTPLLTLPEKRVANFLASQVFPFRLGDPAEVIAHLVOATIE 243		
Db 183 RDLAPIGIRVMTIAPGLFGTPLLTLPEKRVANFLASQVFPFRLGDPAEVIAHLVOATIE 242		
QY 244 PFLNGEVIRLDGAIKMP 261		
Db 243 PFLNGEVIRLDGAIKMP 260		

XX	25-MAR-1999	(first entry)	
DE	Fragment of human secreted protein encoded by gene 8.		
XX	Human; secreted protein; fusion protein; gene therapy; protein therapy;		
KW	diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;		
KW	immunologic abnormality; foetal deficiency; blood; allergy; renal;		
KW	immune system; asthma; lymphocytic disease; brain; hepatitis; lymphoma;		
KW	inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;		
KW	cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;		
KW	osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;		
KW	endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.		
OS	Homo sapiens.		
XX			
XX	WO9842738-A1.		
XX			
PD	01-OCT-1998.		
XX			
PF	19-MAR-1998; 98WC-US05311.		
XX			
PR	30-MAY-1997; 97US-0050937.		
PR	21-MAR-1997; 97US-0041276.		
PR	21-MAR-1997; 97US-0041277.		
PR	21-MAR-1997; 97US-0041281.		
PR	21-MAR-1997; 97US-0042344.		
PR	30-MAY-1997; 97US-0048069.		
PR	30-MAY-1997; 97US-0048094.		
PR	30-MAY-1997; 97US-0048095.		
PR	30-MAY-1997; 97US-0048096.		
PR	30-MAY-1997; 97US-0048099.		
PR	30-MAY-1997; 97US-0048131.		
PR	30-MAY-1997; 97US-0048135.		
PR	30-MAY-1997; 97US-0048154.		
PR	30-MAY-1997; 97US-0048186.		
PR	30-MAY-1997; 97US-0048187.		
PR	30-MAY-1997; 97US-0048188.		
PR	30-MAY-1997; 97US-0048350.		
PR	30-MAY-1997; 97US-0048351.		
PR	30-MAY-1997; 97US-0048352.		
PR	30-MAY-1997; 97US-0048355.		
PR	05-AUG-1997; 97US-0054804.		
XX			
PA	(HUMA-) HUMAN GENOME SCI INC.		
PI	Brewer LA, Duan R, Ebner R, Fierle AM, Florence KA;		
PI	Greene JM, Hu JS, Lallier DW, Moore PA, Ni J, Olsen HS;		
PI	Rosen CA, Rubin SM, Shi Y, Young P;		
XX			
XX	WPI: 1999-070066/06.		
DR	N-PSDB: AAX00618.		
XX			
P1	New isolated human genes and the secreted polypeptides they encode -		
PT	useful for diagnosis and treatment of e.g. cancers, neurological		
PT	disorders, immune diseases, inflammation or blood disorders		
XX			
XX	Disclosure; Page 11; 385pp; English.		
CC	This sequence represents a fragment of a secreted human protein encoded		
CC	by the nucleic acid molecule detailed in the descriptor line. The gene		
CC	can be used to generate fusion proteins by linking to the gene to a		
CC	human immunoglobulin Fc portion (e.g. AAX00602) for increasing the		
CC	stability of the fused protein as compared to the human protein only.		
CC	The invention relates to 87 novel genes and their fragments (nucleic		
CC	acid sequences: AAX00611-X00724; amino acid sequences AAW67807-W68004)		
CC	which are useful for preventing, treating or ameliorating medical		
CC	conditions e.g. by protein or gene therapy. Also, pathological		
CC	polypeptides in a sample or by determining the amount of the new		
CC	polynucleotides. Specific uses are described for each of the 87		
CC	polynucleotides, based on which tissues they are most highly expressed in		

84 267.5 20.5 246 22 AAE02195 S. aureus NADPH-de
85 267 20.5 261 13 AAR7756 NAD affinity gluc
86 267 20.5 276 23 AAY54456 Secoisolaricresin
87 267 20.5 276 23 AAO21494 Secoisolaricresin
88 266 20.4 247 16 AAR66291 Mycobacterium bovi
89 266 20.4 247 16 AAR63899 M. bovis p55 ORF1
90 266 20.4 247 18 AAR40809 M. bovis p55 opero
91 265.5 20.4 268 22 ABB52552 Escherichia coli p
92 265 20.3 272 21 AAB10740 E. megaterium gluc
93 265 20.3 340 21 AAB10741 H. phillipii/B. me
94 264.5 20.3 252 23 AAO16940 Recombinant enzyme
95 264 20.2 243 23 ABB54107 Lactococcus lactis
96 263 20.2 253 22 AAU36249 Pseudomonas aerugi
97 262.5 20.1 273 22 AAY54414 Secoisolaricresin
98 261 20.0 261 23 AAE20115 Lactobacillus rham
99 261 20.0 277 21 AAY54413 Secoisolaricresin
100 260 19.9 261 9 AAB80590 Sequence of glucos

ALIGNMENTS

RESULT 1
AAW71471
ID AAW71471 standard; Protein; 261 AA.

AAW71471;
16-DEC-1998 (first entry)

ERAB protein.

XX Endoplasmic reticulum associated amyloid-beta peptide binding protein;
KW ERAB protein; amyloid-beta peptide; inhibitor; demyelinating disease;
KW neurodegenerative disorder; therapy; Alzheimer's disease; schizophrenia;
KW Down's syndrome; Parkinson's disease; Huntington's disease;
KW Multiple sclerosis.

XX Homo sapiens.

XX WO9840484-A1.

XX 17-SEP-1998.

XX 12-MAR-1998; 98WC-US04915.

XX 12-MAR-1997; 97OS-0815225.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Stern DM, Yan SD;

XX WPI, 1998-531524/45.

XX N-PDB; AAV60576.

XX Endoplasmic reticulum associated amyloid-beta peptide binding
XX protein - inhibitors of which can be used to treat neurodegenerative
XX disorders

XX Claim 2; Fig 1D; 53pp; English.

XX This sequence is the endoplasmic reticulum associated amyloid-beta
XX peptide binding (ERAB) protein of the invention. The protein can be used
XX in a method for evaluating the ability of an agent to inhibit binding of
XX ERAB polypeptide to amyloid-beta peptide comprising: (a) incubating the
XX ERAB polypeptide, the agent and amyloid-beta peptide under binding
XX conditions; (b) determining the amount of amyloid-beta peptide bound to
XX ERAB polypeptide; (c) comparison of the amount of binding with results
XX from a control using no agent, so determining inhibition ability of the
XX agent. The inhibitors identified by the method can be used to treat a
XX neurodegenerative condition by administration of an agent that inhibits
XX binding of an ERAB polypeptide to amyloid-beta peptide, particularly
XX where the disease is Alzheimer's disease, Down's syndrome, Parkinson's

CC disease, Huntington's disease, schizophrenia, a demyelinating disease, or
CC multiple sclerosis. The inhibitors can also be used to treat other
CC neurodegenerative conditions including those associated with ageing,
CC dentatorubral and pallidolysian atrophy, Machado-Joseph disease,
CC muscular dystrophy, senility, spinocerebellar ataxia type I, spinulbar
CC muscular atrophy, stroke, and trauma.
XX

XX Sequence 261 AA;

Query Match 99.7%; Score 1300; DB 19; Length 261;
Best Local Similarity 99.6%; Pred. No. 1,2e-118;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAACRSVKGAVITVGASGLGATAEERLVGAGAVLLDPNSGGEAOKKLNCF 60
DB 1 MAACRSVKGAVITVGASGLGATAEERLVGAGAVLLDPNSGGEAOKKLNCF 60

QY 61 APADVTSKDVOTATLALANGKFGVDVAVNACIAVASTYLUKKQHTTLEDFORVDY 120
DB 61 APADVTSKDVOTATLALANGKFGVDVAVNACIAVASTYLUKKQHTTLEDFORVDY 120

QY 121 NLMTFNVIRLVAGEGONEPPDGGORVINTASVAEFGVGAAVYASKGIVGKTL 180
DB 121 NLMTFNVIRLVAGEGONEPPDGGORVINTASVAEFGVGAAVYASKGIVGKTL 180

QY 181 PIARDLAPIGIRVMTAPGLFGTPLLTSPEKYANFLASQVPPSRKLPAPETAHVQAI 240
DB 181 PIARDLAPIGIRVMTAPGLFGTPLLTSPEKYANFLASQVPPSRKLPAPETAHVQAI 240

QY 241 IENPFLNGEYIRLDGAIKMQP 261
DB 241 IENPFLNGEYIRLDGAIKMQP 261

RESULT 2
AAY32239
ID AAY32239 standard; Protein; 260 AA.

XX AAY32239;

XX 15-FEB-2000 (first entry)

XX Alzheimer-associated beta-amyloid binding protein (ERAB).

XX Alzheimer-associated beta-amyloid binding protein; ERAB; mouse;

XX Leydig cell; differential display RT-PCR; DDRT-PCR;

XX short chain alcohol dehydrogenase; SCAD; testis; marker;

XX spermatogenesis.

XX Mus musculus.

XX

XX Key

XX Location/Qualifiers

XX 10..15

XX /note= "beta sheet region A"

XX 18..32

XX /note= "alpha helix region A"

XX 35..41

XX /note= "beta sheet region B"

XX 43..57

XX /note= "alpha helix region B"

XX 61..66

XX /note= "beta sheet region C"

XX 70..80

XX /note= "alpha helix region C"

XX 84..94

XX /note= "beta sheet region D"

XX 109..133

XX /note= "alpha helix region D"

XX 143..153

XX /note= "beta sheet region E"

XX 167..171

XX /note= "SCAD motif"

XX 165..186

disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. In addition, (1) affects biorythms or circadian cycles of rhythms, fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAU28020-AAU28395 represent novel human secreted protein amino acid sequences of the invention.

Sequence 288 AA;

Query Match 23.0%; Score 300.5; DB 22; Length 288;
Best Local Similarity 29.9%; Pred. No. 5.3e-21;
Matches 84; Conservative 44; Mismatches 110; Indels 43; Gaps 6;

1 MAACRSVKGVLAVITGASGLTAERLYGGAANVLDPNSGGEAAKRLGNNVF 60
10 MAFGRTR-YAQRKAVVATGGRGIGAGIVRAFVNSGARVVICDDSGRLECGCL 68
61 APADVTEKDVOTALALAKRFGKRVDAVNCAGIAVASKTYNLKQOTHTLEDFORVLDV 120
69 SFQCVTEDDVKTIVSTIRFGRIDCVNNAGHPP-----QRPETSAHGFRLL 123
121 NMGTENVIRLVAGEMQNEPDGQGVINTASVAAEFGVGAASAKSGIGVMTL 180
124 NLGTYTLTKLALPYLRSQ-----GVINISLVGALGQAQAVPYATKGAVTAMTK 176
181 PIADLAPIGIRVTIAPGLFGPPLTSLPEKVCNPLASQVPP----- 224
177 ALADESPYGRVVCISPGNIMPLME-----LAALMPDRATIRREGMLAQGRGV 228
225 -----SRIGDPAET-AHLVQAIIENPFLNGEVIRLDGAIRM 259
229 QIQPLGRMGCPAEVGAAYFLASFNCTGIXILVTGAEIL 269

RESULT 24

ABP39667
ID ABP39667 standard; Protein: 263 AA.

AC ABP39667;

DE 24-JUL-2002 (first entry)

Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4512.

Staphylococcus epidermidis: open reading frame: ORF; bacterial infection;

antibacterial; gene therapy.

Staphylococcus epidermidis.

US6380370-B1.

30-APR-2002.

13-AUG-1998; 98US-0134001.

14-AUG-1997; 97US-055779P.

08-NOV-1997; 97US-064964P.

(GENO-) GENOME THERAPEUTICS CORP.

Doucette-Stamm LA, Bush D;

WPI: 2002-381255/41.

N-PSDB; ABN92212.

Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections -

PS Disclosure; SEQ ID 4512; 267pp; English.

ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP3124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site.

Sequence 263 AA;

Query Match 22.5%; Score 295; DB 23; Length 263;
Best Local Similarity 32.3%; Pred. No. 1.6e-20;
Matches 86; Conservative 42; Mismatches 104; Indels 34; Gaps 6;

12 VAVITGASGLTAERLYGGAANVLDPNSGGEAAKRLGNNVFADVTSE 68
11 VAVVGAAGIGLKTAEIRLEFDGYSIALVDREAVAKSAEKLSEGEAVAFRADVSNR 70
69 KDVOTALALAKRFGKRVDAVNCAGIAVASKTYNLKQOTHTLEDFQVLDVNLMTGFNV 128
71 DQVESVLNQVHEHFGDLNVLVNNAGIGPMTPI-----ESVTPQFNQVGVNAGVFWG 124
129 IRLVAGEMQNEPDGQGVINTASVAAEFGVGAASAKSGIGVMTLPIARDLAP 188
125 IOAALIEQF-----DKLGHGKTIINATSQAGVGNAGLSYSTKFAVHGQLVAAARDLAE 179
189 IGIRVVTIAPGLFGPPLTSLPEKVCNPLASQVPP-----SRIGDPAEYA 234
180 KNITVAFAFGIETPMMKGIAX-----LAENNOPMEWGKQFTDQIALKRLSKPEDEVA 235
235 HLVOAII--ENPFLNGEVIRLDGAIR 258
236 NVVSFLAGSDSDYITGOTIIVDGMR 261

RESULT 25

AA683032
ID AA683032 standard; Protein: 262 AA.

AC AA683032;

DE 03-SEP-2001 (first entry)

S. epidermidis open reading frame protein sequence SEQ ID NO:3158.

Staphylococcus epidermidis SRI strain; infection; diagnosis;

Staphylococcus epidermidis.

NO200134809-A2.

17-MAY-2001.

09-NOV-2000; 2000WO-0530782.

09-NOV-1999; 99US-0164258.

(GLAXO) GLAXO GROUP LTD.

Kimmerly WJ;

WPI: 2001-316495/33.

N-PSDB; AAH53882.

Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -


```

XX 25-OCT-2000 (first entry)
DT Bacillus megaterium 3-keto-acyl-CoA reductase Phab.
DE
XX Polyhydroxyalkanoate; polyhydroxybutyrate; transgenic plant; Phab;
KM 3-keto-acyl-CoA reductase.
XX
OS Bacillus megaterium.
XX
PN MO200040730-A1.
XX
PD 13-JUL-2000.
XX
PF 07-JAN-2000; 2000MO-US00364.
XX
PR 07-JAN-1999; 99US-0115592.
XX
PA (UTMA-) UNIV MASSACHUSETTS.
XX
PI Cannon MC, Cannon FC, MCCool GJ, Valentin HE, Gruys KU;
XX
DR WPI: 2000-532624/48.
XX
DR N-PSDB; AAS50142.
XX
PT New nucleic acid fragment encoding proteins involved in
PT polyhydroxyalkanoate (PHA) biosynthesis, useful in the production of
PT transgenic plants or recombinant plant cells which can express PHAs
PT such as polyhydroxybutyrate.
XX
PS Claim 85; page 137-138; 153pp; English.
XX
XX The present sequence is that of Phab, a 3-keto-acyl-CoA-reductase
CC protein of Bacillus megaterium. The sequence was deduced from an
CC open reading frame identified in an isolated 7,916 bp fragment of
CC B. megaterium strain 11561 genomic DNA (see AAS50142). The 7,916 bp
CC DNA fragment includes genes encoding proteins (see AAY95743-47)
CC involved in polyhydroxyalkanoate (PHA) biosynthesis. Nucleic acids
CC encoding these proteins are useful for creating transgenic plants or
CC recombinant host cells which have the capability of expressing PHAs
CC such as polyhydroxybutyrate, polyhydroxyvalerate,
CC polyhydroxyhexanoate, polyhydroxyoctanoate, polyhydroxydecanoate or
CC their copolymers. Claimed methods for preparing a PHA involve
CC obtaining a plant or a cell comprising a nucleic acid encoding
CC a 3-keto-acyl-CoA reductase (especially the present acid sequence), and
CC a nucleic acid encoding a PHA synthase (see AAY95747), and growing
CC the plant or cell under conditions suitable for PHA production.
XX
SQ Sequence 247 AA:

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RESULT 23
AAU28296
ID AAU28296 standard; Protein: 288 AA.
XX
XX AAU28296;
AC
XX
XX 18-DEC-2001 (first entry)
DT
DT
DE Novel human secretory protein, Seq ID No 653.
XX
XX Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
XX Ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
XX transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
XX amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
XX ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
XX gut protection; lung; liver fibrosis; immune deficiency; infection;
XX severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
XX multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
XX fertility; analgesic; pain; antigen.
XX
XX Homo sapiens.
XX
XX MO200166689-A2.
XX
XX 13-SEP-2001.
XX
XX 05-MAR-2001; 2001MO-US04942.
XX
XX 07-MAR-2000; 2000US-0519705.
XX
XX 19-MAY-2000; 2000US-0574454.
XX
XX 17-JUN-2000; 2000US-0596193.
XX
XX 14-JUL-2000; 2000US-0616847.
XX
XX 19-SEP-2000; 2000US-0663563.
XX
XX 20-OCT-2000; 2000US-0693267.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
XX Zhao QA, Yang Y, Dmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
XX
XX WPI: 2001-589934/66.
XX
XX N-PSDB; AAS45196.
XX
XX Novel polypeptides and nucleic acids obtained from cDNA libraries
PT prepared from various human tissues, for diagnosis and treatment of
PT cancer, neurological, inflammatory, and autoimmune disorders.
XX
XX Example 2; SEQ ID No 653; 107pp; English.
XX
XX The invention relates to novel isolated human secreted polypeptides (I)
XX and polynucleotides (II). (I) and (II) are useful for treating
XX inflammatory conditions such as arthritis, nephritis, Crohn's disease,
XX ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
XX involved in increasing haematopoiesis, stem cell survival, bone growth
XX and remodelling. (I), (II) and modulators of (II) are useful for
XX prophylaxis or treatment of one or more cancers. (II) is also useful for
XX creating transgenic animals useful for studying the in vivo activities of
XX the polypeptide as well as for studying modulators of the polypeptides.
XX (I) induces the proliferation of neural cells and regeneration of nerve
XX and brain tissue and is useful for the treatment of central and
XX peripheral nervous system diseases and neuropathies, such as Alzheimer's,
XX Parkinson's disease, Huntington's disease, and amyotrophic lateral
XX sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
XX activity, regulation of haematopoiesis and is useful for treating myeloid
XX or lymphoid cell disorders, platelet disorders such as thrombocytopenia
XX and for regeneration of bone, cartilage, tendon, ligament and/or nerve
XX tissue growth, and in tissue repair, healing of burns, incisions,
XX ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
XX disorders, or periodontal disease. Furthermore, (I) is also useful for
XX gut protection or regeneration and treatment of lung or liver fibrosis,
XX reperfusion injury in various tissues, various immune deficiencies and

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PR 05-APR-1999; 99JP-0098205.
 XX (DAIL) DAICEL CHEM IND LTD.
 XX
 XX Yamamoto H;
 PI
 XX WPI, 2000-118183/11.
 DR N-PSDB; AA245749.
 PT Producing optically pure (S)-4-halo-3-hydroxybutyric acid ester -
 XX
 PS Claim 6: Page 19-20; 34pp; English.
 XX
 CC The present sequence represents a beta-ketoacyl-ACP reductase protein
 CC of *Bacillus subtilis*. The beta-ketoacyl-ACP reductase enzyme constitutes
 CC a type II fatty acid synthetase. The enzyme has an extremely high
 CC reducing activity and stereoselectivity towards 4-chloroacetoacetic
 CC acid ester. The specification describes a method for producing a
 CC (S)-4-halo-3-hydroxybutyric acid ester. The method comprises
 CC asymmetrically reducing 4-halo-acetoacetic acid ester or its
 CC derivative with beta-ketoacyl-acyl carrier protein reductase
 CC constituting type II fatty acid synthase, or acetoacetyl-coA
 CC reductase constituting the polypeptide hydroxy fatty acid biosynthesis
 CC system. The novel method is used to produce optically active
 CC 4-halo-3-hydroxybutyric acid ester, with a high purity.
 CC
 XX Sequence 248 AA;
 SQ
 Query Match 23.7%; Score 310.5; DB 21; Length 248;
 Best Local Similarity 29.7%; Pred. No. 4.0e-22;
 Matches 76; Conservative 55; Mismatches 100; Indels 25; Gaps 6;
 OY 13 AVINGASGIGLATAEERLVGQASAVLLDLPNSGGEAQA-----KILGNCVFAPADY 65
 DB 9 AIVTGAAGRGIRSLALALAKSAGNV---VNSGNEKANEVDEIKSMGRKAIKADY 65
 OY 66 TSEEDVOTALLAKGKGRVDVAVNCAGIVASKTYLKGQCHTLEDFORVLDVLMGT 125
 DB 66 SNPDVONMKIKETLSVFSTIDILVNNAGITRDMIMRKE-----DEMDDVINILKGV 119
 OY 126 FNVIRLVAGEGONEPDGQGVITINTASVAAFEQGVQGAASASKSGIVGMLPIARD 185
 DB 120 FNCIKATYROMKQ-----RSGRIIVSSIVGVSGMPGQANVYAKAYIGLTKSSAKE 173
 OY 186 LAPGIRVMTAPLEGFTPLITSLEPKYCNFLASQVFPFRLDPAVIAHLVQAIIEN-- 243
 DB 174 LASNIITVNAIAPGFISTDMTKLAKVODEMKQIPL-ARFGSPDSVSSVTFILASEGA 232
 OY 244 PFLNGEIVRLDGAIRM 259
 DB 233 RYMTGQTLHIDGKVM 248

XX 11-APR-2000; 2000FR-0004629.
 PR (INSP) INST PASTEUR.
 XX
 XX Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
 PI Dussurgeat O, Chetoui F, Nedjari H, Glaser P, Kunst F, Cossart P;
 PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JB;
 PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
 PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
 PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
 PI Madueno E, De Pablos B, Wehlund J, Kaerst U, Entian K, Hauf J;
 PI Rose M, Voss H;
 DR WPI, 2002-010914/01.
 XX
 CC Genomic sequence for *Listeria monocytogenes*, useful e.g. for treatment
 CC and prevention of *Listeria* and related bacterial infections, and
 CC related polypeptides -
 XX
 PS Claim 6, SEQ ID No 1597, 192pp; French.
 XX
 CC The present invention relates to the genome sequence of *Listeria*
 CC monocytogenes Egd-e (see ABA03041). The genome sequence and fragments of
 CC it are useful for selecting probes and primers for detecting genes in *L.*
 CC monocytogenes and related organisms, and for studying genetic
 CC polymorphisms and other genomes. The present sequence is a protein
 CC encoded by the genome sequence of the present invention. Proteins
 CC expressed from the genome sequence are useful for raising specific
 CC antibodies, identification of *L. monocytogenes* and related organisms, and
 CC for biosynthesis and biodegradation, especially biosynthesis of vitamin
 CC B12. The genome sequence and proteins encoded by it are also useful for
 CC selecting compounds that regulate gene expression and cell replication
 CC and modulate *L. monocytogenes*-related diseases. In addition, the genome
 CC sequence and proteins encoded by it are useful in pharmaceutical and
 CC vaccine compositions for the treatment or prevention of infections by *L.*
 CC monocytogenes and related organisms.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at http://wipo.int/pub/published_pct_sequences.
 CC
 XX Sequence 247 AA;
 SQ
 Query Match 23.2%; Score 303.5; DB 23; Length 247;
 Best Local Similarity 32.0%; Pred. No. 2.2e-21;
 Matches 85; Conservative 45; Mismatches 103; Indels 33; Gaps 7;
 OY 7 SVKGLVAVITGGASGIGLATAEERLVGQASAVLLDLPNSGGEAQA-----KKL---GNNC 58
 DB 2 TLQGRVAVVTGSGRIGRIDIAINLAKEGANIRF---VYNSGPEAAETAKLVAEHGEV 57
 OY 59 VFAPADYSEKDVQATALLAKGKFGVVDVAVNCAGIVASKTYNKKKGQCHTLEDFORVL 118
 DB 58 EAKKAVVAIAEDVDFAFFKQAIERFGRVDILVNNAGITRDMIMRKE-----DEMDDVI 111
 OY 119 DVNLGCTFNVIRLVAGEGONEPDGQGVITINTASVAAFEQGVQGAASASKSGIVGM 178
 DB 112 NINIKGTFICTRAVSRFMKQ-----RAGKIINNASVVLGIGNGOANVYASKAGVIGL 165
 OY 179 TLPIDARDLAPIGIRVMTAPLEGFTPLITSLEPKYCNFLASQVFPFRLDPAVIAHLVQ 238
 DB 166 TKTTAKELAPRGIVNNAVAPGFITTDMTKDKLEKREMLAQIP---LGAIGTEDIAN 221
 OY 239 AII-----ENPFLNGEIVRLDGAIRM 259
 DB 222 AVLFLASDASKYITGQTLISVDGKVM 247

RESULT 21
 ABB48892
 ID ABB48892 standard; Protein: 247 AA.
 XX
 AC ABB48892;
 XX
 XX 05-FEB-2002 (first entry)
 DE *Listeria monocytogenes* protein #1596.
 XX
 KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
 KW vitamin B12; bacterial infection; disease.
 XX
 OS *Listeria monocytogenes*.
 XX
 PN WO200177335-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 11-APR-2001; 2001WO-FR01118.

RESULT 22
 AAY95746
 ID AAY95746 standard; Protein: 247 AA.
 XX
 AC AAY95746;

OS Pyrococcus abyssi.
 XX
 FN FR2792651-A1.
 XX
 PD 27-OCT-2000.
 XX
 PF 21-APR-1999; 99FR-0005034.
 XX
 PR 21-APR-1999; 99FR-0005034.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 PI (IFRE-) IFREMER INST FR RECH EXPL MER.
 FI Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O;
 PI Querellou J, Weissenbach J, Saurin W, Hellig R;
 XX WPI; 2001-126236/14.
 DR
 XX
 PT New nucleotide sequences isolated from Pyrococcus abyssi encode
 PT proteins useful in industry.
 XX
 PS Claim 7; Pages 1087-1088; 1657pp; French.
 XX
 CC The present invention relates to the genomic sequence of Pyrococcus
 CC abyssi (see AAF66431 and AAB41223-7) and P. abyssi proteins. P. abyssi is
 CC a hyperthermophilic archaeon, which is isolated from deep-sea
 CC hydrothermal vents. The present sequence is one such P. abyssi protein.
 CC The proteins of the present invention have various potential industrial
 CC uses, since the proteins are stable at very high temperatures, some up to
 CC 110 degrees centigrade.
 CC Note: This patent is in the same patent family as WO2000065062, which
 CC contains additional sequences as shown in AAB99132-AAB99143,
 CC AAB95903-AAH75920 and AAG66436.
 CC
 XX
 SQ Sequence 241 AA;
 Query Match 23.9%; Score 313.5; DB 22; Length 241;
 Best Local Similarity 35.3%; Pred. No. 2.3e-22;
 Matches 91; Conservative 44; Mismatches 88; Indels 35; Gaps 8;
 QY 8 VKGIIVAVTGGASGLGATARIIVGCGASAVILDLPSGGPAOKKRGNNC-----VF 60
 DB 4 LKGVAVLTGASRIGRAIAIEIAKRGVAVYINRSN---EEAKKTEELCRQYGVETLL 60
 QY 61 APAVTVSEKDYOTALALAKGFGFVAVVAVNCGIYAVASKTYNKKGGTHLEDFQRYLDV 120
 DB 61 VKADVSNREEVREVKVYDKFGRIDILINNAGI--LGKT---KDPLEVTDEEDRVISV 115
 QY 121 NLMTGFVIRIYVADMGQNEPDGQGVIIINTASVAFEGVQGAAYASKSGIYVMTL 180
 DB 116 NLKGAFTYTOGVLYRM-----KKGKIVNINISIGKGGVIGVPHYASKGGLIALTF 166
 QY 181 PIARDLPIGIRVITAPGLTGLTLLSLPEKVCNFIASQVPEPSRIGD--PAFYAHLY 237
 DB 167 NLAHILAP-NITLVANAVAPGPDVDTMLSEKMKMLKTL-----SLGDIAPKPEVAHAV 218
 QY 238 QAIENPFLNGEVIRLDG 255
 DB 219 IFLLENHITGEVIDVNG 236
 RESULT 18
 AAU28156 ID AAU28156 standard; Protein: 237 AA.
 XX
 AC AAU28156;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secretory protein, Seq ID No 325.
 XX
 KM Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KM tschaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;

KM transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 KM amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
 KM ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KM gut protection; lung; liver fibrosis; immune deficiency; infection;
 KM severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
 KM multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 KM fertility; analgesic; pain; antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200166689-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 05-MAR-2001; 2001WO-US04942.
 XX
 PR 07-MAR-2000; 2000US-0519705.
 PR 19-MAY-2000; 2000US-0574454.
 PR 17-JUN-2000; 2000US-0596193.
 PR 14-JUL-2000; 2000US-0616847.
 PR 19-SEP-2000; 2000US-0665363.
 PR 20-OCT-2000; 2000US-0693267.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
 PI Zhao QA, Yang Y, Dmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
 DR WPI; 2001-589934/66.
 DR N-PSDB; AAS45056.
 PT Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders -
 XX
 PS Example 4; SEQ ID No. 325; 107pp; English.
 XX
 CC The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischemia-reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing hematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I), (II) and modulators of (II) are useful for
 CC propylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions, and
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
 CC analgesic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAU28020-AAU28395 represent novel human secreted protein
 CC amino acid sequences of the invention.
 XX
 SQ Sequence 237 AA;

Matches	82; Conservative	42; Mismatches	110; Indels	26; Gaps	5
QY	5	CRSRKGIYAVITGGASGIGLTAETAEIVYQGSAYVLDLPNSGGEGQAOKKLGNCVYFAPAD	64		
Db	17	CDSEMDKCAVCAFGSGSRGIGRAVADLMARKYRLAVIARNEGAKAAADLGDDHAFSCD	76		
QY	65	VTSEKDVQATALAKGKFGRYDVAVNCAGI-----AVASKTYNKKGQTHLEDFQRYLD	119		
Db	77	VAKEHDVQNTPEEMEKHLGRVNEFLVNAGINRDGLVFTXT-----EDWVSQHL	125		
QY	120	VNLGTEFVILVAGEMQNEPDGQGVIIINASVAFEGQVQGAAYASAKSGIVGCT	179		
QY	126	TNLGSMITCCAAAMRTIQ-----QGGSIVNGSIVGLGNSQSVYSASGGLVGS	179		
Db	180	LPIARDLAPIGIRVWTIAPGEGFPLTSLPEKYCNFLASQVFPSPSRIGDPAEYAHLYQA	239		
Db	180	RALKAEVARKIRVAVVAFGEVHTMDLKEE--HLKKNIPL-GREGETIEVAHAAYF	235		
QY	240	IIENPUNGVIYRLDGAIRM	259		
Db	236	LIESPYITGHVLYVDGGIQL	255		
RESULT	16				
ID	AAM50255				
XX	AAM50255 standard; Protein; 237 AA.				
AC	AAM50255;				
XX					
DT	21-JAN-2002 (first entry)				
XX					
DE	Human dehydrogenase 21509.				
XX					
KW	Dehydrogenase; human; ovarian cancer; colon cancer; lung cancer;				
KW	liver cancer; metastasis; antitumor; therapy; diagnosis.				
XX					
OS	Homo sapiens.				
XX					
Key	Location/Qualifiers				
FT	Domain	3..229			
FT	/note="short-chain alcohol dehydrogenase domain"				
FT	Region	148..158			
FT	/note="short-chain alcohol dehydrogenase family signature"				
FT	Modified-site	114..116			
FT	/note="O-phosphorylated by protein kinase C"				
FT	Modified-site	66..69			
FT	/note="O-phosphorylated by casein kinase II"				
FT	Modified-site	95..98			
FT	/note="O-phosphorylated by casein kinase II"				
FT	Modified-site	9..14			
FT	/note="N-myristoylated"				
FT	Modified-site	38..43			
FT	/note="N-myristoylated"				
FT	Modified-site	110..115			
FT	/note="N-myristoylated"				
FT	Modified-site	128..133			
FT	/note="N-myristoylated"				
FT	Modified-site	134..139			
FT	/note="N-myristoylated"				
FT	Modified-site	153..158			
FT	/note="N-myristoylated"				
XX					
PN	WO200175119-A2.				
XX					
PD	11-OCT-2001.				
XX					
PF	02-APR-2001; 2001WO-US10720.				
XX					
PR	31-MAR-2000; 2000US-193920P.				
XX					
PA	(MILL-) MILLENNIUM PHARM INC.				
XX					

```

PI Meyers RA, Rudolph-Owen LA;
DR WPI: 2001-626438/72.
DR N-PSDB; RA170573.
XX
XX Novel isolated 21509 and 33770 polypeptides belonging to human
PT dehydrogenase family members, useful for treating cancer, diabetes,
PT atherosclerosis, glomerulonephritis, Crohn's disease, cirrhosis,
PT multiple sclerosis -
XX
XX Claim 1(a); Fig 2; 146pp; English.
PS
XX
XX The present sequence is that of a novel human dehydrogenase,
CC designated 21509. The protein has a significant number of
CC structural characteristics in common with members of the
CC dehydrogenase/oxido-reductase family. Its expression pattern
CC suggests a role in tumour development. The invention provides
CC 21509 and 33770 nucleic acids, antisense molecules, recombinant
CC expression vectors, host cells and transgenic animals in which a
CC 21509 or 33770 gene has been introduced or disrupted. It also
CC provides 21509 and 33770 proteins, fusion proteins, antigenic
CC peptides and antibodies, and methods for screening for compounds
CC that modulate the expression or activity of 21509 or 33770
CC polypeptides or nucleic acids. Such modulators are used in methods
CC for inhibiting the proliferation or migration, or inducing the
CC killing, of 21509- or 33770-expressing cells, especially the
CC hyperproliferative and/or metastatic cells of a soft tissue tumour,
CC solid tumour or metastatic lesion, especially ovarian cancer, colon
CC cancer, lung cancer and liver cancer (claimed). Modulator
CC compounds are also used in claimed methods of modulating fatty acid
CC biosynthesis or retinoid biosynthesis in a cell. 21509 and 33770
CC nucleic acids can also be used to prepare diagnostic probes and in
CC gene (including antisense) therapy.
XX
XX
XX Sequence 237 AA:
SQ
XX
XX Query Match 24.0%; Score 314; DB: 22; Length 237;
XX Best Local Similarity 32.0%; Pred. No. 2e-22;
XX Matches 81; Conservative 41; Mismatches 105; Indels 26; Gaps 5
XX
XX 12 VAVITGASGSLTAERLVYOGASAVLLDIPNSGSGEQAQKLGNNCYFAPADVTSERDV 71
XX | | | | | : : : : : : : : : : : : : : : : : : : : :
XX 4 VCAIGGSRGIGRAVAQQLMARGVLLAIARLLEGAKAAGDUGDHLAFSCDVAKEHDV 63
XX
XX 72 QTALLAAGKGRVDVAVNCAGI-----AVASKTYNLAKKGQHTLEDQRLVDVLMGTF 126
XX | | | | | : | | | | | : : : : : : : : : : : : : : :
XX 64 QNTFEMKRGHGRVFLVNAAGINDSLVLRKT-----EDWVSQLHTVLLDSM 112
XX
XX 127 NVIRLVAGEMGNENPDGQGRGVIIINTASVAFAFGQVQAQYASAKSGIVGNTLPIDRL 186
XX : : : : : : : : : : : : : : : : : : : : : : : : :
XX 113 LTCKAAMAMIQ-----QGGSIVNAGSIVGLKNGSCQSYASAKSGIVGFSRALAKEV 166
XX
XX 187 APIGIRVNTAPGLGFTPLNLSLPKVCNFTLASQVFPFSRIGDPRAVEHIVGAIINENPL 246
XX | | | | | : | | | | | : | | | | | : | | | | | : | | |
XX 167 ARKRIKRVAVAGVFNHTDKLEE---HLKKNIP-LGRGETTEVAHAVVFLLESPTI 222
XX
XX 247 NGEVIRLDGAIIM 259
XX | : | : | : :
XX 223 TGHVAVDGLQL 235
XX
XX
XX RESULT 17
XX AAB96397
XX AAB96397 standard; Protein; 241 AA.
XX
XX AAB96397;
XX
XX 29-OCT-2001 (first entry)
XX
XX Putative P. abyssal dehydrogenase #8.
XX
XX Hypertrophic archaean; hypertrophic protein.
XX

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XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GT;
PI Yamamoto RT, Xu HH;
XX WPI: 2001-611495/70.
DR N-PSDB; AAS53187.
XX
PT New polynucleotides for the identification and development of
XX antibiotics, comprise sequences of antisense nucleic acids -
PS Example 3; Seq ID No 10921; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequences is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 245 AA;
Query Match 24.3%; Score 318.5; DB 22; Length 245;
Best Local Similarity 33.7%; Pred. No. 7.5e-23;
Matches 84; Conservative 38; Mismatches 108; Indels 19; Gaps 5;
QY 15 ITGASGLGLATLAEVLVGGASAVLVD---LPSNGGEAQAATLGNVCVAPADVASEKD 70
DB 10 ITGSTRIGRAVALAFKAGKAGNYLVNRSRITPEQREITA--FGKCTISDSDIDPDA 67
QY 71 VQNALALAKGFGKGVDAVAVACAGVASKYNNKKGQTHLEDFQRYLVNMGKTNVIR 130
DB 68 AGEMIQATVQDGLGIDILVNAGIT-----NKLILRMKEPFNCIDINLGTFTNMG 121
QY 131 LVASGMQNEPDGSGGVITINTASVAFEGVGQAAYASKSGIYGMTPIARDAPIG 190
DB 122 QAVRRMKQ-----RGRILLMASVSGLMGNVQANYSKAGVGFTSVAREVAPRG 175
QY 191 IRVATLAPGLFETPLTSLPEKYCNFLASQVPEPSRLDPAEYAHVLAQIINPEFLNGEV 250
DB 176 ITCAVALPFGFQTEMTDVLSEKVTQNNAOIPLOT-FGVEDVAAFAIFLAKSPYITGV 234
QY 251 IRLDGLIRM 259
DB 235 VNVDSGLVM 243
XX
DE Novel human secretory protein, Seq ID No 701.
XX
KW Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
KW Ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
KW Transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
KW Amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;

KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
KW gut protection; lung; liver fibrosis; immune deficiency; infection;
KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
KW fertility; analgesic; pain; antigen.
XX
OS Homo sapiens.
XX
PN W020016689-A2.
XX
PD 13-SEP-2001.
XX
PF 05-MAR-2001; 2001WO-US04942.
XX
PR 07-MAR-2000; 2000US-0519705.
XX
PR 19-MAY-2000; 2000US-0574454.
XX
PR 17-JUN-2000; 2000US-0596193.
XX
PR 14-JUL-2000; 2000US-0616847.
XX
PR 19-SEP-2000; 2000US-0665363.
XX
PR 20-OCT-2000; 2000US-0693267.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YF, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
XX
DR WPI: 2001-589934/66.
DR N-PSDB; AAS45244.
XX
PT Novel polypeptides and nucleic acids obtained from cDNA libraries
PT prepared from various human tissues, for diagnosis and treatment of
PT cancer, neurological, inflammatory, and autoimmune disorders -
PS Example 2; SEQ ID No 701; 107pp; English.
XX
XX The invention relates to novel isolated human secreted polypeptides (I)
XX and polynucleotides (II). (I) and (II) are useful for treating
XX inflammatory conditions such as arthritis, nephritis, Crohn's disease,
XX ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
XX involved in increasing haematopoiesis, stem cell survival, bone growth
XX and remodeling. (I), (II) and modulators of (II) are useful for
XX prophylaxis or treatment of one or more cancers. (II) is also useful for
XX creating transgenic animals useful for studying the in vivo activities of
XX the polypeptide as well as for studying modulators of the polypeptides.
XX (I) induces the proliferation of neural cells and regeneration of nerve
XX and brain tissue and is useful for the treatment of central and
XX peripheral nervous system diseases and neuropathies, such as Alzheimer's,
XX Parkinson's disease, Huntington's disease, and amyotrophic lateral
XX sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
XX activity, regulation of haematopoiesis and is useful for treating myeloid
XX or lymphoid cell disorders, platelet disorders such as thrombocytopenia
XX and for regeneration of bone, cartilage, tendon, ligament and/or nerve
XX tissue growth, and in tissue repair, healing of burns, incisions,
XX ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
XX disorders, or periodontal disease. Furthermore, (I) is also useful for
XX gut protection or regeneration and treatment of lung or liver fibrosis,
XX reperfusion injury in various tissues, various immune deficiencies and
XX disorders including severe combined immunodeficiency (SCID), bacterial or
XX fungal infections, autoimmune disorders e.g. multiple sclerosis,
XX rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
XX reactions and conditions, such as asthma or other respiratory problems.
XX In addition, (I) affects biorythms or circadian cycles of rhythms,
XX fertility, metabolism, catabolism, anabolism, storage or elimination of
XX dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
XX analgesic effects or other pain reducing effects, immunoglobulin like
XX activity and can act as an antigen in a vaccine composition to raise an
XX immune response. AAU28020-AAU28395 represent novel human secreted protein
XX amino acid sequences of the invention.
XX
SQ Sequence 257 AA;
Query Match 24.2%; Score 317; DB 22; Length 257;
Best Local Similarity 31.5%; Pred. No. 1.1e-22;

XX Streptococcus pneumoniae.
OS
XX WO200044885-A1.
XX
XX 03-AUG-2000.
XX
XX 19-JAN-2000; 2000WO-US01131.
XX
XX 27-JAN-1999; 99US-0239052.
XX
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX
XX Holmes DJ, Mooney J, Zhong YY, Debouck C, Jaworski DD, Wang M;
PI Warren RL, Kosmatka AL, McDevitt D, Ingraham KA, Chalker AF;
PI So CY, Wallis NG, Pearson SC;
XX
XX WPI: 2000-482971/42.
XX
XX N-PSDB: AAA74684.
XX
XX FabG polypeptide, isolated from Streptococcus pneumoniae, is used to
PT treat microbial diseases, identify agonists and antagonists for
PT treating microbial infections and to detect diseases associated with
PT microbial infections -
XX
XX Claim 1; Page 3; 40pp; English.
XX
XX The present sequence is a FabG (2-oxoacyl-acyl carrier protein
CC reductase) polypeptide. A full length fabg gene was isolated from a
CC Streptococcus pneumoniae 0100993 DNA library in E. coli. FabG
CC polynucleotides and polypeptides are used for detection and treatment of
CC microbial diseases. They may also be used to identify antagonists and
CC agonists which can then be used to treat microbial diseases. Compounds
CC that interfere with the initial physical interaction between a pathogen
CC and a host have been identified. The compounds are able to prevent the
CC adhesion of bacteria to mammalian extracellular proteins in wounds,
CC prevent adhesion between mammalian extracellular proteins and bacterial
CC FabG proteins which mediate tissue damage and/or to block normal
CC progression of pathogenesis in infections mediated by implantation of
CC in-dwelling devices or other surgical techniques. The FabG
CC polypeptides, polynucleotides, antagonists and agonists are especially
CC useful in the treatment of Helicobacter pylori infection. They may be
CC used to decrease H. pylori-induced cancers and to prevent, inhibit
CC and/or cure gastric ulcers and gastritis.
XX
XX Sequence 243 AA:
SO
Query Match 24.9%; Score 326.5; DB 21; Length 243;
Best Local Similarity 35.1%; Pred. No. 1.2e-23;
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;
OY 15 ITGASGSLGATFARLVGQASAVLIDLPNSGGE-----AQAKKGNKCFAPADVTSE 68
DB 10 ITGSSRSGIGLAIHKAFAQAGANTVL---NSRGAISEELAEFSNYGIKVPISGDVSDF 65
OY 69 KDVOATLALAKGTRGVAVNCAGIAVASKTYNLKKGQHTLEDFORVLDVNLGTFNV 128
DB 66 ADARMRIDQALAEISGVAVLVNNGI--TQDTLMKKM---TEADFEVLEKVNLTGAFNM 119
OY 129 IRLVAGGEGNEPDGQGGQRYITNTASVAAFEQGVGAASASGAGVGMFLPARDIAP 188
DB 120 TQSVL-----KPMKAREGAIINNSVVGIMNGINQANVYASAGLIGFTKSVAREVAA 173
OY 189 IGIRMTIAPGLGFTPLTSLPEKVCNPLASQVFPSPSLGDPAEVAHLVQAIINPPLNG 248
DB 174 RNIRNVNAPGMIEDMALLSDIKKENTLQIIM-KFQGAQEVADLTVFLAQDYLITG 232
OY 249 EYIRLDGAIKM 259
DB 233 QVIAIDGGLSM 243
RESULT 10

AAU37767
ID AAU37767 standard; Protein; 243 AA.
XX
XX AAU37767;
XX
XX 14-FEB-2002 (first entry)
XX
XX Streptococcus pneumoniae cellular proliferation protein #196.
XX
XX Antisense; prokaryotic cellular proliferation protein;
XX antibiotic; antibacterial; drug design.
XX
XX Streptococcus pneumoniae.
XX
XX WO200170955-A2.
XX
XX 27-SEP-2001.
XX
XX 21-MAR-2001; 2001WO-US09180.
XX
XX 21-MAR-2000; 2000US-191078P.
XX
XX 23-MAY-2000; 2000US-206848P.
XX
XX 26-MAY-2000; 2000US-207727P.
XX
XX 23-OCT-2000; 2000US-242578P.
XX
XX 27-NOV-2000; 2000US-253625P.
XX
XX 22-DEC-2000; 2000US-257931P.
XX
XX 16-FEB-2001; 2001US-269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Hasselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GT;
PI Yamamoto RT, Xu HH;
XX
XX WPI: 2001-611495/70.
XX
XX N-PSDB: AAS55626.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
PT
XX
XX Example 3; Seq ID NO 13360; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pcl_sequences.
XX
XX Sequence 243 AA:
SO
Query Match 24.9%; Score 326.5; DB 22; Length 243;
Best Local Similarity 35.1%; Pred. No. 1.2e-23;
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;
OY 15 ITGASGSLGATFARLVGQASAVLIDLPNSGGE-----AQAKKGNKCFAPADVTSE 68
DB 10 ITGSSRSGIGLAIHKAFAQAGANTVL---NSRGAISEELAEFSNYGIKVPISGDVSDF 65
OY 69 KDVOATLALAKGTRGVAVNCAGIAVASKTYNLKKGQHTLEDFORVLDVNLGTFNV 128

XX New Streptococcus protein for the treatment or prevention of infection
PT or disease caused by Streptococcus bacteria, such as meningitis, and
PT for detecting a compound that binds to the protein -
PS Claim 1, Page 3542; 4525bp; English.

XX The invention relates to a protein (ABP25413-ABP30895) from group B
CC Streptococcus/SBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (SI), given in
CC the specification. The proteins have antibacterial and anti-inflammatory
CC activity. (I), nucleic acids encoding (I), AB66044-ABN71526 and
CC antibodies that bind (I) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (I) are used to detect Streptococcus in a
CC biological sample. (I) is used to determine whether a compound binds to
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (I) may be used to recombinantly produce (I) and may be
CC used in gene therapy. Antibodies to (I) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins.

XX Sequence 243 AA:

SO Sequence 243 AA:

Query Match 26.8%; Score 351; DB 23; Length 243;
Best Local Similarity 35.4%; Pred. No. 5e-26;
Matches 92; Conservative 42; Mismatches 100; Indels 26; Gaps 6

QY 8 VKGLAVITGGASGLATLAEVLVQGSAYVLDLPNSGGEAQAKT-----GNNCYF 60
DB 3 IKGNI :FIIIGSTRGIGLMAHQFASLEANIYL-----NGRSAISEEIVASHFTDGYVVT 56
QY 61 APADVSEKDVOTALAKGFRGVDAVNVAGTAVASKVTNLKGGTHLTEDFORLDV 120
DB 57 ISADVSEAEAKRMVNEALIESGIDVLYNNAGIT-----NDKLMLKMEDEPERVLT 110
QY 121 NMGSTENVIRLVAGEMGONEDPDQSGQKSVIINTASVAAEFSGVQGAAYSASKGIVGML 180
DB 111 NLGGAENMTQSYL-----KPMIKARQGAIIWSSVGLTNGINQANYAASKMGMTGFTK 164
QY 181 PIKRDAPIGIRMTAPGLFTPLTSLPEKVCFTLASQVFPFSRLDPAEVAHLVQAI 240
DB 165 SVAREYAAKNTCYNAIAPGFISSDMTGVLPKMQDQIIISQILPM-KRIGKQAEVAHLASF 223
QY 241 IENPFLNGEYIRLDGAIRMQ 260
DB 224 VEDDYITGQVIAIDGGMWQ 243

RESULT 8
ID AAM80670 standard; Protein; 243 AA.
AC AAM80670:
XX
XX 24-DEC-1998 (first entry)
XX
XX S. pneumoniae fatty acid biosynthesis protein.
XX
XX Streptococcus pneumoniae protein; recombinant; gene expression; DNA chip;
XX virulence; antibody; infection; detection; treatment; hypothetical;
XX cell wall biosynthetic; external target; minimal gene set protein.
OS Streptococcus pneumoniae.
XX
XX WO9826072-A1.
XX
XX 18-JUN-1998.
XX
XX 09-DEC-1997; 97WO-US22578.

```

XX PR 13-DEC-1996: 9605-0036281.
XX XX
XX PA (EHLI ) LILLY & CO EHLI.
XX PI Baltz RH, Burgett SC, Detoff BS, Hoskins JA, Jaakunas SR;
XX PI Mills BU, Norris FH, Peery RB, Rocky FK, Rostock FR;
XX PI Skatard PL, Smith MC, Solenberg PU, Treadway PU;
XX PI Young Bellido ML;
XX DR WPI, 1998-348529/30.
XX
XX PT Streptococcus pneumoniae nucleic acid sequences - used in DNA chips
XX PT for evaluating gene expression, and identification of virulence
XX PS genes
XX PS
XX PS Claim 3; Page 270; 333pp; English.
XX
XX CC This sequence represents a S. pneumoniae fatty acid biosynthesis
XX CC protein. The invention provides DNA sequences (AAV65201 to AAV65204)
XX CC from the Streptococcus pneumoniae genome and corresponding protein
XX CC sequences (AAW60605 to AAW60728). The protein sequences are classified as
XX CC hypothetical, cell wall biosynthetic, external target, or minimal gene
XX CC set proteins. A recombinant host containing a vector comprising any of
XX CC the above nucleic acids can be used for the recombinant expression of the
XX CC proteins. The invention also provides a DNA chip having arrayed on it at
XX CC least 15 base pair fragment of any one or more of these DNA sequences.
XX CC The DNA chip can be used methods for evaluating gene expression in S.
XX CC pneumoniae and for identifying virulence genes in S. pneumoniae.
XX CC Antibodies that selectively bind to the above proteins or peptide
XX CC fragments can be used to treat S. pneumoniae infection. The antibodies
XX CC can also be used to detect S. pneumoniae cells.
XX
XX SQ Sequence 243 AA:
XX
XX Query Match 24.9%; Score 326.5; DB 19; Length 243;
XX Best Local Similarity 35.1%; Pred. No. 1,2e-23;
XX Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6
XX
OY 15 ITGAGAGLGLATRIERIVGGASAVLLDLPNSGGF-----AQAKKLGNCFAPADYISE 68
DB 10 ITGSSSRIGIATLHKRAKQAGANIV----NSRGALISEELAEFSNYIKVPISSGVDSF 65
OY 69 KDVOTATLAKGKFGVDVAVNCAGIAVASKTYNLKGGOTHTLDFORVLDVLMKGFENV 128
DB 66 ADARKMIDQAIALISGVDTLVNNAGI--TDTLMLKKM---TEADPEKYVLTGAFNM 119
OY 129 IRLVAGMGONEDDGGQAGVIITNASTVAATEGGVGAAYASNGGIVGHTLPIARDLP 188
DB 120 TQSVL-----KPMKARKGAIINNSVYGLMGNGQANVYASRAGLIGFTKSVAREVAS 173
OY 189 IGIRVMTIAPGLEGTPLTSLPEKCNFLASQVPPSPSLDPAPYAHVLAQIENFPLNG 248
DB 174 RNIRVNVYIAGMIESMTAILSDKIKENTIAQIPR-KRFGGAEQVADLVTFLAGQDYLVG 232
OY 249 EYIRLDGAIKRM 259
DB 233 QVIAIDGGLSM 243
XX
XX RESULT 9
XX ID AAB15706
XX AAB15706 standard; Protein; 243 AA.
XX
XX AC AAB15706;
XX
XX DT 07-DEC-2000 (first entry)
XX
XX DE Streptococcus pneumoniae FagB polypeptide.
XX
XX KW Streptococcus pneumoniae; FagB; 3-oxoacyl-acyl carrier protein reductase;
XX Helicobacter; cytostatic; antitumor; cancer; gastric ulcer; gastritis;
XX Helicobacter pylori infection; microbial infection.

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Query Match 50.8%; Score 664.5; DB 18; Length 388;
 Best Local Similarity 55.5%; Pred. No. 2,36-56;
 Matches 141; Conservative 35; Mismatches 69; Indels 9; Gaps 3;

QY 8 VKGLVAVITGGASGLGATLAEKLVGGASAVLLDLPNSGGEAQAQKKGNNCVRADPDTYS 67
 DB 143 IEGRFVAVTGAASGLGASAVLLDLPNSGGEAQAQKKGNNCVRADPDTYS 196
 QY 68 EKDVOIALALAKGFRVDVAVNCAGIYASVSKTYNKKQTHLEDFQRYLDVNLMTGFN 127
 DB 197 ATAGOTAFALATDFGRDLGVLNCGAGIAPARM--LGRDPHGIDSTFARAVTINLISFN 254
 QY 128 VIRLVAGEMGONEPDGQGRGVITNTASVAAFEQVQQAAYSASKGIVGNTPIARDLA 187
 DB 255 MARLAELMARNEFVR--GERGVIVNTASIAADQIGQVAYVASKACVAGMTLPMARDLA 313
 QY 188 PIGIRVMTIAPGLTPTLLTSLPEKVCNFLASQVFPSPRLGDPAEVAHLVQATIEENFELN 247
 DB 314 RHGIRVMTIAPGIRTPLEBGLPDQVDSLGAAVFPFSRLGEPSEYALHLHITANPMN 373
 QY 248 GEVIRLDGATIMQ 261
 DB 374 GEVIRLDGATIMQ 387

RESULT 6
 ABP28011
 ID ABP28011 standard; Protein: 244 AA.
 AC ABP28011;
 DE 02-JUL-2002 (first entry)
 DE Streptococcus polypeptide SEQ ID NO 5198.
 DE Streptococcus polypeptide SEQ ID NO 5198.
 KM Streptococcus; GAS; group B streptococcus; Streptococcus agalactiae;
 KM group A streptococcus; Streptococcus pyogenes; antibacterial;
 KM antiinflammatory; infection; vaccine; meningitis; gene therapy.
 OS Streptococcus agalactiae.
 XX WO200234771-A2.
 XX 02-MAY-2002.
 XX 29-OCT-2001; 2001WO-GB04789.
 XX 27-OCT-2000; 2000GB-0026333.
 PR 24-NOV-2000; 2000GB-0028727.
 PR 07-MAR-2001; 2001GB-0005640.
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 PI Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
 PI Tetelin H;
 DR WPI; 2002-352536/38.
 DR N-PSDB; ABN68642.
 XX New Streptococcus protein for the treatment or prevention of infection
 PT or disease caused by Streptococcus bacteria, such as meningitis, and
 PI for detecting a compound that binds to the protein -
 XX Claim 1; Page 3863; 4525pp; English.
 CC The invention relates to a protein (ABP25413-ABP30895) from group B
 CC Streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (SI), given in
 CC the specification. The proteins have antibacterial and antiinflammatory
 CC activity. (I), nucleic acids encoding (I), ABN6044-ABN71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for

CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a
 CC biological sample. (I) is used to determine whether a compound binds to
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins.

Sequence 244 AA:
 Query Match 27.6%; Score 361.5; DB 23; Length 244;
 Best Local Similarity 36.5%; Pred. No. 4,76-27;
 Matches 92; Conservative 38; Mismatches 99; Indels 23; Gaps 5;

QY 15 ITGASGLGATLAEKLVGGASAVLLDLPNSGE-----AQAKKGNNCVRADPDTSE 68
 DB 10 ITGSSRGIGLAIHQFQJGANTVL---NGRSEISETLAEFADYGVKVIISGDVSSF 65
 QY 69 KDVOIALALAKGFRVDVAVNCAGIYASVSKTYNKKQTHLEDFQRYLDVNLMTGFNV 128
 DB 66 EDANRMKEALIASLGSVDVLVNNAGIT-----NDKLMKMTVEDESVLXINTGAFYM 119
 QY 129 IRLVAGEMGONEPDGQGRGVITNTASVAAFEQVQQAAYSASKGIVGNTPIARDLP 188
 DB 120 TGSVL-----KMTARQGAIIINISSVGLTGNVQAVYASKALIGFTSVAREVA 173
 QY 189 IGIRVMTIAPGLTPTLLTSLPEKVCNFLASQVFPSPRLGDPAEVAHLVQATIEENFELN 248
 DB 174 RGIRVMTIAPGLTPTLLTSLPEKVCNFLASQVFPSPRLGDPAEVAHLVQATIEENFELN 232
 QY 249 EVIRLDGATIMQ 260
 DB 233 QVIAIDGGMTO 244

RESULT 7
 ABP27345
 ID ABP27345 standard; Protein: 243 AA.
 AC ABP27345;
 DE 02-JUL-2002 (first entry)
 DE Streptococcus polypeptide SEQ ID NO 3866.
 DE Streptococcus polypeptide SEQ ID NO 3866.
 KM Streptococcus; GAS; group B streptococcus; Streptococcus agalactiae;
 KM group A streptococcus; Streptococcus pyogenes; antibacterial;
 KM antiinflammatory; infection; vaccine; meningitis; gene therapy.
 OS Streptococcus pyogenes.
 XX WO200234771-A2.
 XX 02-MAY-2002.
 XX 29-OCT-2001; 2001WO-GB04789.
 XX 27-OCT-2000; 2000GB-0026333.
 PR 24-NOV-2000; 2000GB-0028727.
 PR 07-MAR-2001; 2001GB-0005640.
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 PI Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
 PI Tetelin H;
 DR WPI; 2002-352536/38.
 DR N-PSDB; ABN67976.

Query Match 87.4%; Score 1144; DB 21; Length 260;
 Best Local Similarity 87.6%; Pred. No. 2.2e-103;
 Matches 226; Conservative 18; Mismatches 14; Indels 0; Gaps 0;

QY 4 ACRSVKGVAVITGASGLGATLAEKLVGOGASAVLLDLPNSGGAQAKKIGNNCYFAPADVS 63
 DB 3 AVRSKGLVAVITGASGLGATLAEKLVGOGATVAVLDVPSGGAQAKKIGSCIFAPA 62
 QY 64 DVTSEKDVOTALAKKGFGRVDVAVNCAGIYAVASKTYNLRKQTHLEDFORVLDVNL 123
 DB 63 NVTSEKEIOAALTAKKFGRIIDVAVNCAGIYAVIKTYHOKKNIHTLEDFORVNL 122
 QY 124 GFENVIRLVAGEMGQNEPDGQGRGVIINTASVAAFEQVGOAAVSASKGIYGMTLP 183
 DB 123 GFENVIRLVAGEMGQNEPDGQGRGVIINTASVAAFEQVGOAAVSASKGIYGMTLP 182
 QY 184 RDLAIGIRVMTIAPGLFGLTSLPEKVCNFIASQVPPSRUGDPAEYAHVQALITEN 243
 DB 183 RDLAIGIRVMTIAPGLFGLTSLPEKVCNFIASQVPPSRUGDPAEYAHVQALITEN 242
 QY 244 PFLNGEVIRLDGAIKMP 261
 DB 243 PFLNGEVIRLDGAIKMP 260

RESULT 4

ABR62988 standard; Protein; 255 AA.

ID ABR62988 standard; Protein; 255 AA.
 AC ABR62988;
 DT 26-MAR-2002 (first entry)
 XX Drosophila melanogaster polypeptide SEQ ID NO 15756.
 DE Drosophila melanogaster polypeptide SEQ ID NO 15756.
 KM Drosophila melanogaster polypeptide; cell signalling; insecticide;
 KW pharmaceutical.
 OS Drosophila melanogaster.
 XX WO200171042-A2.
 PN 27-SEP-2001.
 XX 23-MAR-2001; 2001WO-US09231.
 PE 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI; 2001-656860/75.
 DR N-PSDB; ABL07091.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PT Disclosure; SEQ ID NO 15756; 21pp + Sequence Listing; English.
 PS The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins
 CC (AB57737-AB872072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 255 AA;
 SQ

Query Match 69.4%; Score 908; DB 22; Length 255;
 Best Local Similarity 68.9%; Pred. No. 2.3e-80;
 Matches 175; Conservative 29; Mismatches 50; Indels 0; Gaps 0;

QY 8 VKGLVAVITGASGLGATLAEKLVGOGASAVLLDLPNSGGAQAKKIGNNCYFAPADVS 67
 DB 2 IRNNAVSVITGASGLGATLAEKLVGOGASAVLLDLPNSGGAQAKKIGNNCYFAPADVS 61
 QY 68 EKDVOTALAKKGFGRVDVAVNCAGIYAVASKTYNLRKQTHLEDFORVLDVNLGTFN 127
 DB 62 EKDVSAALQAKKGFGRVDVAVNCAGIYAVASKTYNLRKQTHLEDFORVLDVNLGTFN 121
 QY 128 VIRLVAGEMGQNEPDGQGRGVIINTASVAAFEQVGOAAVSASKGIYGMTLP 187
 DB 122 VIRLVAGEMGQNEPDGQGRGVIINTASVAAFEQVGOAAVSASKGIYGMTLP 181
 QY 188 PIGIRVMTIAPGLFGLTSLPEKVCNFIASQVPPSRUGDPAEYAHVQALITEN 247
 DB 182 TQIRICTIAPGLFGLTSLPEKVCNFIASQVPPSRUGDPAEYAHVQALITEN 241
 QY 248 GEVIRLDGAIKMP 261
 DB 242 GEVIRLDGAIKMP 255

RESULT 5

AAW06513 standard; Protein; 388 AA.

ID AAW06513 standard; Protein; 388 AA.
 AC AAW06513;
 DT 08-MAR-1997 (first entry)
 XX Flavobacterium ORF-5 gene product.
 DE Flavobacterium ORF-5 gene product.
 KM Carotenoid; lycopene; beta-carotene; echinenone; canthaxanthin;
 KW zeaxanthin; adonixanthin; astaxanthin.
 OS Flavobacterium sp. R1534 WT (ATCC 21586).
 XX EP747483-A2.
 PN 11-DEC-1996.
 PE 29-MAY-1996; 96EP-0108556.
 PR 09-JUN-1995; 95EP-0108888.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PA Hohmann H, Pasamontes L, Tessier M, Van Loon A;
 PI WPI; 1997-023160/03.
 DR N-PSDB; AAT45143.
 XX Flavobacterium gene sequences encoding carotenoid biosynthesis
 PT enzymes - for the production of carotenoid(s), useful in foods and
 PT animal feeds
 PT Example 2; Fig 7; 80pp; English.
 PS A polypeptide (AAW06513) showing approx. 30% homology to
 CC streptomycete polypeptide synthases was identified as the product
 CC of ORF-5 from a carotenoid gene cluster (see also AAT45143) of
 CC Flavobacterium sp. R1534. 5 Other open reading frames of the
 CC gene cluster coded for carotenoid biosynthetic enzymes (see also
 CC AAW06515-18 and AAW00871) and can be used to produce carotenoids in
 CC transformed host cells.
 XX Sequence 388 AA;
 SQ

84	265.5	20.3	246	22	AAE02195	S. aureus NADPH-de
85	265.5	20.3	268	22	AB852552	Escherichia coli p
86	264	20.2	247	16	AA866291	Mycobacterium bovis
87	264	20.2	247	16	AA838899	M. bovis p55 ORF1
88	264	20.2	247	18	AA40809	M. bovis p55 opero
89	264	20.2	276	21	AA54416	Secoisolaricresin
90	264	20.2	276	23	AA021494	Secoisolaricresin
91	263	20.1	261	13	AA827756	NAD affinity gluc
92	262.5	20.1	252	23	AA016940	Recombinant enzyme
93	261	19.9	277	21	AA810740	B. megaterium gluc
94	261	19.9	277	21	AA54413	Secoisolaricresin
95	261	19.9	340	21	AA810741	H. ghiliani/B. me
96	260.5	19.9	273	21	AA54414	Secoisolaricresin
97	260	19.9	253	23	AB854107	Lactococcus lactis
98	259	19.8	253	22	AA036249	Pseudomonas aerugi
99	258	19.7	283	21	AA031552	Arabidopsis thalia
100	258	19.7	283	23	AB892823	Herbicidally activ

ALIGNMENTS

RESULT 1
AAW71471
ID AAW71471 standard; Protein: 261 AA.

AAW71471;

16-DEC-1998 (first entry)

ERAB protein.

Endoplasmic reticulum associated amyloid-beta peptide binding protein;

ERAB protein; amyloid-beta peptide; inhibitor; demyelinating disease;

neurodegenerative disorder; therapy; Alzheimer's disease; schizophrenia;

Down's syndrome; Parkinson's disease; Huntington's disease;

multiple sclerosis.

Homo sapiens.

MO9840484-A1.

17-SEP-1998.

12-MAR-1998;

98WO-US04915.

12-MAR-1997;

97US-0815225.

(UYCO) UNIT COLUMBIA NEW YORK.

Stern DM, Yan SD;

MP1, 1998-531524/45.

N-PSDB; AAV60576.

Endoplasmic reticulum associated amyloid-beta peptide binding

protein - inhibitors of which can be used to treat neurodegenerative

disorders

Claim 2; Fig 1D; 53pp; English.

This sequence is the endoplasmic reticulum associated amyloid-beta

peptide binding (ERAB) protein of the invention. The protein can be used

in a method for evaluating the ability of an agent to inhibit binding of

ERAB polypeptide to amyloid-beta peptide comprising: (a) incubating the

ERAB polypeptide, the agent and amyloid-beta peptide under binding

conditions; (b) determining the amount of amyloid-beta peptide bound to

ERAB polypeptide; (c) comparison of the amount of binding with results

from a control using no agent, so determining inhibition ability of the

agent. The inhibitors identified by the method can be used to treat a

neurodegenerative condition by administration of an agent that inhibits

binding of an ERAB polypeptide to amyloid-beta peptide, particularly

where the disease is Alzheimer's disease, Down's syndrome, Parkinson's

CC disease, Huntington's disease, schizophrenia, a demyelinating disease, or
CC multiple sclerosis. The inhibitors can also be used to treat other
CC neurodegenerative conditions including those associated with ageing,
CC dentatorubral and pallidolysian atrophy, Machado-Joseph disease,
CC muscular dystrophy, senility, spinocerebellar ataxia type I, spinulbar
CC muscular atrophy, stroke, and trauma.
XX

SO Sequence 261 AA;

Query Match 100.0%; Score 1309; DB 19; Length 261;

Best Local Similarity 100.0%; Pred. No. 1.7e-119; Mismatches 0; Gaps 0;

Matches 261; Conservative 0; Indels 0; Gaps 0;

QY 1 MAACRSVGLVAVINGGASGLIATAEERLVGQASAVLDDPNSGGEAOKLGNVCF 60

Db 1 MAACRSVGLVAVINGGASGLIATAEERLVGQASAVLDDPNSGGEAOKLGNVCF 60

QY 61 APADVTSEKDVOTALALAKGFRVDVAVNCAGIAVASKTYNLKKQHTLEDFOFVLDV 120

Db 61 APADVTSEKDVOTALALAKGFRVDVAVNCAGIAVASKTYNLKKQHTLEDFOFVLDV 120

QY 121 NLKGTFFNVRIVLAVGEGQNEPDGQGRVITNTASVAAFEQVQAAASASGIVGML 180

Db 121 NLKGTFFNVRIVLAVGEGQNEPDGQGRVITNTASVAAFEQVQAAASASGIVGML 180

QY 181 PIARDIAPIGIRVMTIAPGLFETPLTSLPERVCNPLASQVFPRLGDPAYAAHLYQAI 240

Db 181 PIARDIAPIGIRVMTIAPGLFETPLTSLPERVCNPLASQVFPRLGDPAYAAHLYQAI 240

QY 241 IENPFLNGEYIRLDGAIKMP 261

Db 241 IENPFLNGEYIRLDGAIKMP 261

RESULT 2
AAW67934
ID AAW67934 standard; Protein: 227 AA.

AAW67934;

25-MAR-1999 (first entry)

Fragment of human secreted protein encoded by gene 8.

Human; secreted protein; fusion protein; gene therapy; protein therapy;

diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;

developmental abnormality; foetal deficiency; blood; allergy; renal;

immune system; asthma; lymphocytic disease; brain; hepatitis; lymphoma;

inflammation; ischaemic shock; Alzheimer's disease; stenosis; AIDS;

cognitive disorder; schizophrenia; prostate; obesity; osteoclasts; thymus;

osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;

endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

Homo sapiens.

WO9842738-A1.

01-OCT-1998.

19-MAR-1998;

98WO-US05311.

30-MAY-1997;

97US-0050937.

21-MAR-1997;

97US-0041276.

21-MAR-1997;

97US-0041277.

21-MAR-1997;

97US-0041281.

21-MAR-1997;

97US-0042344.

30-MAY-1997;

97US-0048096.

30-MAY-1997;

97US-0048095.

30-MAY-1997;

97US-0048096.

30-MAY-1997;

97US-0048099.

30-MAY-1997;

97US-0048131.

30-MAY-1997;

97US-0048135.

Thu Jun, 26 06:55:11 2003

us-09-931-186-8.rag

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:19:21 ; Search time 39.6667 Seconds

(without alignments)
876.767 Million cell updates/sec

Title: US-09-931-186-8
Perfect score: 1309
Sequence: 1 MAACRSVKGLVAITIGAS.....ENPFLNGEYIRLDGAIKMP 261

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A:Geneseg_101002.*
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23: /SID52/gcgdata/geneseg/genesegp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1309	100.0	261	19	AAW617931
2	1146	87.5	227	20	AAW61934
3	1144	87.4	260	21	AAW32239
4	908	69.4	255	22	ABW82988
5	664.5	50.8	388	18	AAW06513
6	361.5	27.6	244	23	ABP28011
7	351	26.8	243	23	ABP27345
8	326.5	24.9	243	19	AAW06070
9	326.5	24.9	243	21	AAW15706
10	326.5	24.9	243	22	AAU37767

11	326.5	24.9	243	22	AAU37988	Streptococcus pneu
12	325.5	24.9	243	22	AAW01032	CPE 35 protein seq
13	324.5	24.8	243	22	ABW54087	Lactococcus lactis
14	318.5	24.3	245	22	AAU53328	Enterococcus faeca
15	317	24.2	257	22	AAU28344	Novel human secret
16	314	24.0	237	22	AAW50255	Human dehydratogen
17	313.5	23.9	241	22	AAW66397	Human dehydratogen
18	312	23.8	237	22	AAW28156	Putative P. abysci
19	312	23.8	237	22	AAW19928	Novel human secret
20	310.5	23.7	248	21	AAW54422	Human oxidoreducta
21	303.5	23.2	247	23	ABW48892	Amino acid sequenc
22	301	23.0	247	21	AAW95746	Listeria monocylog
23	300.5	23.0	288	22	AAU28296	Bacillus megaterium
24	295	22.5	263	23	ABP39667	Novel human secret
25	294	22.5	262	22	AAW83032	Staphylococcus epi
26	293.5	22.4	267	22	AAW47459	S. epidermidis ope
27	292.5	22.3	262	22	AAW86537	Levodione reductas
28	291	22.2	315	17	AAW89323	G. suboxydans DSM
29	291	22.2	315	17	AAW89322	Rape leaf beta-ket
30	290.5	22.2	270	20	AAW41761	Human PRO474 prote
31	290.5	22.2	270	21	AAW44317	Human PRO474 (UNOS
32	290.5	22.2	270	21	AAW44317	Human PRO474 (UNOS
33	290.5	22.2	270	22	AAW28108	Human PRO474 prote
34	290.5	22.2	279	22	AAU18296	Novel human secret
35	289.5	22.1	244	21	AAW54421	Human endocrine po
36	289.5	22.1	244	22	AAW34533	Amino acid sequenc
37	288.5	22.0	246	12	AAW10974	E. coli cellular p
38	288.5	22.0	262	21	AAW44578	Acetoacetyl CoA re
39	288	22.0	263	22	AAW38499	Xylytol dehydrogen
40	287.5	22.0	246	10	AAW94157	Salmonella typhi c
41	287.5	22.0	246	14	AAW32192	Acetyl-CoA reducta
42	287.5	22.0	246	20	AAW43310	Sequence encoded b
43	287.5	22.0	246	21	AAW54423	Acetoacetyl-CoA re
44	287.5	22.0	246	22	AAW71981	Amino acid sequenc
45	287.5	22.0	303	23	ABW92824	Relistia eutropha
46	287.5	22.0	329	16	AAW71224	Herbicideally activ
47	286.5	21.9	270	21	AAW42558	Acetyl-CoA-reducta
48	286.5	21.9	277	21	AAW42558	Human OREP ORF232
49	283.5	21.7	253	23	ABW54415	Seobolactaricresin
50	283.5	21.6	273	10	AAW94155	Lactococcus lactis
51	282	21.5	280	23	ABW92449	Acetyl-CoA reducta
52	280.5	21.4	254	22	AAW49773	Herbicideally activ
53	280.5	21.4	306	22	AAW81544	Protein with acety
54	279.5	21.4	241	12	AAW10679	S. epidermidis ope
55	278.5	21.3	242	12	AAU05950	Acetoacetyl CoA re
56	278.5	21.3	243	23	ABP39886	Propionibacterium
57	277	21.2	274	22	AAW81518	Staphylococcus epi
58	276	21.1	258	22	AAW92482	Human AFP protein
59	276	21.1	258	22	AAW92482	C glutamincum prote
60	276	21.1	285	22	AAW34448	Corynebacterium gl
61	275	21.0	285	22	AAW34448	E. coli cellular p
62	274.5	21.0	246	14	AAW47461	Acetoacetyl CoA re
63	274.5	21.0	254	22	AAW47461	(R)-2-octanol dehy
64	274	20.9	269	23	ABW92448	Herbicideally activ
65	273.5	20.9	206	23	AAW92445	Short-chain dehydr
66	273	20.9	249	23	ABP39980	Staphylococcus epi
67	272.5	20.8	242	23	AAW77210	Staphylococcus epi
68	272.5	20.8	286	22	AAW36267	Consensus protein
69	271.5	20.7	286	22	AAW36267	Staphylococcus aur
70	269.5	20.6	251	22	AAW34193	Pseudomonas aerugi
71	269.5	20.6	246	21	AAW15707	Staphylococcus aur
72	269.5	20.6	246	22	AAW33965	Staphylococcus aur
73	269.5	20.6	246	22	AAW36530	Staphylococcus aur
74	269.5	20.6	246	22	AAU37210	Staphylococcus aur
75	269.5	20.6	246	22	AAU37210	Staphylococcus aur
76	268.5	20.5	231	23	ABP39852	Staphylococcus aur
77	268.5	20.5	248	20	AAW36959	Staphylococcus epi
78	267.5	20.4	186	19	AAW38474	Chlamydia trachoma
79	266.5	20.4	336	16	AAW06488	S. pneumoniae 3-Ox
80	266.5	20.4	242	22	AAW35381	Matze T52 sequence
81	266.5	20.4	266	21	AAW92509	Human hemophilus influe
82	266.5	20.4	307	21	AAW35504	Human OXRE-6 Hom
83	266	20.3	254	23	ABW48207	Arabidopsis thalia
			23			Listeria monocylog

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Search completed: June 23, 2003, 14:35:42
Job time : 13.1667 secs

us-09-931-186-8.ra1

Page 12

REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 270:
SEQUENCE CHARACTERISTICS:
LENGTH: 186 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6348328e
US-08-858-207A-270

Query Match 20.5%; Score 268; DB 4; Length 186;
Best Local Similarity 38.7%; Pred. No. 5.8e-22;
Matches 74; Conservative 23; Mismatches 72; Indels 22; Gaps 5;

QY 15 ITGGASGIGLATAERLYGOGASAVLLDLPNSGGE-----AQAKKIGNCVFAPADVTSE 68
DB 10 ITGSSRGIGLAIAMKFAQAGANIVL-----NSRGAISELLAFPSNIGIKVYPIGSDVSDF 65
QY 69 KDVOFTALALAKGKGRDVAVNCAGIYASKTYNLKKGQTHLEDFOFVLDVNLMTFNV 128
DB 66 ADARMTDQALAEISYDVLVNNGI--TODTLMLKM---TEADFEKVLKVLNLTGAFFM 119
QY 129 IRLVAGEMGONPDGOGGVYINTASVAEFGVGQAAYSASKGIVGMLPIARDLAP 188
DB 120 TQSVL-----KPMKARREGALIMSSVGMIGQANTAAKAGLIGTTKVARRYAS 173
QY 189 IGIRVMTIAPG 189
DB 174 RIRVNTIAPG 184

RESULT 24
US-08-440-856A-3
Sequence 3, Application US/08440856A
Patent No. 5750873

GENERAL INFORMATION:
APPLICANT: DELAPORTA, STEPHEN L.
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: KORIISON & FOENSTER
STREET: 2000 PENNSYLVANIA AVE. N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20037

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,856A
FILING DATE: 15-MAY-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 05463-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1517
TELEFAX: (202) 887-0763
TELEX: 706141
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
US-08-440-856A-3

Query Match 20.4%; Score 267.5; DB 1; Length 337;
Best Local Similarity 30.9%; Pred. No. 1.7e-21;
Matches 88; Conservative 44; Mismatches 112; Indels 41; Gaps 6;

QY 6 RSVKGLAVITGGASGIGLATAERLYGOGASAVLLDLPNSGGEAQAKKIGNCVFAPADY 65
DB 51 KRDKGRVAIVTGGARGIGEAIVLEPAKHGARVIADIDDAAGALASALGPOVSPVRDQV 110
QY 66 TSEKDVOTLALAKGE--GRVDVAVNCAGIYASKTYNLKKGQTHLEDFOFVLDVNLMTG 124
DB 111 SVEDDVRAAVDVALSHSGRLDYCCNNAGV--LGRQTRARSLTSPDAEFDFVRLVNLG 169
QY 125 TENVILVAGEMGONPDGOGGVYINTASVAEFGVGQAAYSASKGIVGMLPIAR 184
DB 170 AALGKHAARAPR-----RAGSLVSAVAAYLGLGPHAYASKHATVGLTKNAAC 223
QY 185 DIAPIGIRVMTIAPGLFTPL-----TSLP-----EK 212
DB 224 ELRAHGVRYNCSPFVATPMLINAROGHDATAADRDLDLDVYVPSDQEVKEKME 283
QY 213 VCNFLASQVPPSRIGDPAEYALVQALLENPFLNGEYIRLDGAI 257
DB 284 VVGLATLKGPTLRPRDIAE--AVLFLASDEARYISGHNLVVDGCV 327

RESULT 25
US-09-504-358-14
Sequence 14, Application US/09504358
Patent No. 6365376

GENERAL INFORMATION:
APPLICANT: Rouviere, Pierre E.
TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIA
FILE REFERENCE: BC1001 US NA
CURRENT APPLICATION NUMBER: US/09/504,358
EARLIER FILING DATE: 2000-02-15
EARLIER APPLICATION NUMBER: 60/120,702
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Microsoft Office 97
SEQ ID NO 14
LENGTH: 256
TYPE: PRT
ORGANISM: Brevibacterium sp HCU
US-09-504-358-14

Query Match 20.3%; Score 266; DB 4; Length 256;
Best Local Similarity 30.9%; Pred. No. 1.6e-21;
Matches 82; Conservative 39; Mismatches 116; Indels 28; Gaps 8;

QY 10 GLVAVITGGASGIGLATAERLYGOGASAVLLDLPNSGGEAQAKL---GNNCVFAPADVT 66
DB 6 GKVAIVITGGAAGRIOSELYASEGQAVVDVNEQEGRAFADATRASGVANVWKLDVS 65
QY 67 SENDVOTLALAKGKGRDVAVNCAGIYASKTYNLKKGQTHLE--DFQVLDVNLMTG 124
DB 66 DESEVEIVSDIAKRGALVNLNAGVGAOK-----PHEIDRLDLVLVSDVKG 118
QY 125 TENVILVAGEMGONPDGOGGVYINTASVAEFGVGQAAYSASKGIVGMLPIAR 184
DB 119 VEFMTHCIPFKQ---AGG--GALVNFASLYGLVSGEELTPYAAKAAVVALTKQAV 172
QY 185 DIAPIGIRVMTIAPGLFTPLTSLEK-----VCNFLASQVPPSRIGDPAEY--AH 235
DB 173 TYGPNIRVNAVAPGILTPLVKEGSRGPDGLDGYTKMGAKHPL--GVGTPEEVAAT 231
QY 236 LVQALLENPFLNGEYIRLDGAI 260
DB 232 LFLASEASFTIGAVLPVDGQYTAQ 256

FILING DATE: 13-AUG-1990
 APPLICATION NUMBER: 67,695
 FILING DATE: 29-JUN-1987
 SEQ ID NO: 4
 LENGTH: 273
 5512669-4

Query Match 21.6%; Score 282.5; DB 6; Length 273;
 Best Local Similarity 31.5%; Pred. No. 2.5e-23;
 Matches 90; Conservative 42; Mismatches 91; Indels 63; Gaps 11;

12 VAVITGASGLGATTAERLVGQASAVLLDLPNSGEAQAQKLNCCVAPA-----63
 4 VALVTGSGRGIG-----AAISIALKAGAYKAAASYAGNDAAKPFKAETGIAY 51
 64 ---DVTSEKDVOTALLAKKGFGRVDVAVNCAGIATAVASKTYNKKGQTH--TLEDPRVL 118
 52 YKMDVSTIEACVEGIAKAEADLGFTDVLVNNAGIT-----KDAHFHKMTPOQNAVI 103
 119 DVNLGTFENVL-----RLV-----AGEMGQ-NEPDQGOR---GVYIN 152
 104 NTNLGLFNMTHPVWSGMRDSFGRIYVSSINGQKGQMGANYSVMSGRHDSFGRIYV 163
 153 TASVAAREGQVGOAAYSAKSGIGVMTLPRIARDLAPIGIRVMTIAPGLFGLTSLPEK 212
 164 ISSINGQKGQMGQANYSAKAGDVGFTKALAQESAAKGTIVNAICPGYIGTEWYRAIPEK 223
 213 VCN-FLASQVFPFRLGDPAAEYAHV--QAIENPFLNGEVIRLDG 255
 224 VLNERIIPQIV-GRLGEPDEIARIYVFLASDEAGFITGSIISANG 268

RESULT 18
 US-09-134-001C-4431
 ; Sequence 4431, Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134,001C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/064,964
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR APPLICATION NUMBER: US 60/055,779
 ; PRIOR FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 5674
 ; SEQ ID NO 4431
 ; LENGTH: 274
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-4431

Query Match 21.3%; Score 278.5; DB 4; Length 274;
 Best Local Similarity 31.7%; Pred. No. 7.1e-23;
 Matches 85; Conservative 45; Mismatches 93; Indels 45; Gaps 8;

12 VAVITGASGLGATTAERLVGQASAVLLDLP-----NSGGEAQAQKLNCCV 60
 10 IAVITGASTGIGASAVALLAEGAHVALDISDLEETVQSINDNGKATYRV-----63
 61 APADYTSKDVOTALLAKKGFGRVDVAVNCAGIATAVASKTYNKKGQTH--TLEDPRVL 118
 64 ---DISDQVKQKSEKIAOEFGRVDFVFNAGVNGA-----GRHEPVEVPEKIM 113
 119 DVNLGTFENVIRLVAGEMQNEPDQGORVITNTASVAAREGQVGOAAYSAKSGIGVMT 178
 114 AVDMGTLVYKFL-----PLMKQGGSIINTASSGAAALYRSGYVMAAGVYINF 166
 179 TLPIARDIAPGIRVMTIAPGLFGLTSLPEKVCNFLASQ--VEPFRLDGPA 231
 167 TKSIAIEYGRNIRANAIAPGTIETPIVDNLGTSDEBAGCTFRENCKWVYPLGRLGPD 226

QY 232 EYAHVQ--AIENPFLNGEVIRLDGAI 257
 DB 227 EVGKLVAFLLASDSSFTGTETIRIDGV 254

RESULT 19

US-09-134-001C-4825
 ; Sequence 4825, Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
 ; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134,001C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/064,964
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR APPLICATION NUMBER: US 60/055,779
 ; PRIOR FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 5674
 ; SEQ ID NO 4825
 ; LENGTH: 249
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-4825

Query Match 20.9%; Score 273.5; DB 4; Length 249;
 Best Local Similarity 29.1%; Pred. No. 2.2e-22;
 Matches 74; Conservative 54; Mismatches 105; Indels 21; Gaps 6;

13 AVITGASGLGATTAERLVGQASAVLLDLPNSGEAQA-----KRLGNCCVAPADVTS 67
 10 ALVTGASRGIGRSIALQLAEEGYN-VAVYAGSKDKAEAVEIEKAGVESPAIQANVAK 68
 68 EKDVOTALLAKKGFGRVDVAVNCAGIATAVASKTYNKKGQTHLEDPRQVLDVNLGTFN 127
 69 GDEVKEMIKVVSQFSGVDVAVNNAGITDKNLLMRKE-----QEMDVDTNKKGVFN 122
 128 VIRLVAGEMQNEPDQGORVITNTASVAAREGQVGOAAYSAKSGIGVMTLPRIARDIA 187
 123 CIQKVPQMLRQ-----RSGAIINTLSIYAGANGNGQANYATKAGVIGLRTAREDA 176
 188 PIGIRVMTIAPGLFGLTSLPEKCNFLASQVPEPFRLDGPAEYAHVQAIEN--PE 245
 177 SRGITVNAVAPGFTVSDMTNALSDDLKQMLEQIPL-KRFGEDTIANTVAPLASPKAY 235
 246 LNGEVIRLDGAIEM 259
 236 ITGOTIHVNGMYM 249

RESULT 20

US-09-238-481-2
 ; Sequence 2, Application US/09238481
 ; Patent No. 6110704
 ; GENERAL INFORMATION:
 ; APPLICANT: Huang, Jiansheng
 ; APPLICANT: McDevitt, Daniel
 ; TITLE OF INVENTION: Fabs
 ; FILE REFERENCE: GM10192
 ; CURRENT APPLICATION NUMBER: US/09/238,481
 ; CURRENT FILING DATE: 1999-01-28
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 246
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-238-481-2

Query Match 20.6%; Score 269.5; DB 3; Length 246;

APPLICATION NUMBER: 08/562,114
FILING DATE: 22-No. 6280997ember-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/375,962
FILING DATE: 20-January-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/258,418
FILING DATE: 10-June-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6280997man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5372.3
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]reductase
NAME/KEY:
US-08-729-594A-13

Query Match 21.8%; Score 285.5; DB 4; Length 244;
Best Local Similarity 29.6%; Pred. No. 9.8e-24;
Matches 75; Conservative 50; Mismatches 113; Indels 15; Gaps 4;
QY 9 KGLVAVITGGASGLTAEFLVVGASAVLLDLPNSGGEAOKKLGNNCFAPADVTSE 68
DB 4 EKKALVTVGASRGIGRAIETLARGKVIQTATSENGAQAISDYLGANGKGLMLNVTDP 63
QY 69 KDVOITALAKKRGKRDVAVNCAGIYASKTYNLKKGGTHLEDFORVLDVNLMGTFNY 128
DB 64 ASIESVLEKIRAEFGVDILVNNAGITRDNLMLMKD-----EWMNDIIEINLSSVRL 117
QY 129 IRLVAGEMQNEPDGGQGVIIINTASVAAFEQGVQGAAYSASKSGIVGMLPIARDLAP 188
DB 118 SKAVRAMMK-----RHGRITIGSVVGTMGNGGQANAAKAGLIGFSKSLAREVAS 171
QY 189 IGIWYTIAPGLFGFTPLTSLPEKVCNPLASQVPPSRLDGPAEYAHLYQ--AIENPFL 246
DB 172 RGIIVNVVAPGFETIDMTRLSDDQAGILAOVP-AGRLGGAQEIANNVAVFLASDEAYI 230
QY 247 NGEVIRLDGALRM 259
DB 231 TGETLHVNGMYM 243
RESULT 16
US-08-937-993-13
Sequence 13, Application US/08937993
Patent No. 6399344
GENERAL INFORMATION:
APPLICANT: Eriksan, Olaf Simon, Andras; Romet, Anna
TITLE OF INVENTION: ISOLATED PROTEINS HAVING CIS-R
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,993

FILING DATE: September 26, 1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/729,594
FILING DATE: 11-October-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/562,114
FILING DATE: 22-No. 6399344ember-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6399344man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5517
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]reductase
NAME/KEY:
US-08-937-993-13

Query Match 21.8%; Score 285.5; DB 4; Length 244;
Best Local Similarity 29.6%; Pred. No. 9.8e-24;
Matches 75; Conservative 50; Mismatches 113; Indels 15; Gaps 4;
QY 9 KGLVAVITGGASGLTAEFLVVGASAVLLDLPNSGGEAOKKLGNNCFAPADVTSE 68
DB 4 EKKALVTVGASRGIGRAIETLARGKVIQTATSENGAQAISDYLGANGKGLMLNVTDP 63
QY 69 KDVOITALAKKRGKRDVAVNCAGIYASKTYNLKKGGTHLEDFORVLDVNLMGTFNY 128
DB 64 ASIESVLEKIRAEFGVDILVNNAGITRDNLMLMKD-----EWMNDIIEINLSSVRL 117
QY 129 IRLVAGEMQNEPDGGQGVIIINTASVAAFEQGVQGAAYSASKSGIVGMLPIARDLAP 188
DB 118 SKAVRAMMK-----RHGRITIGSVVGTMGNGGQANAAKAGLIGFSKSLAREVAS 171
QY 189 IGIWYTIAPGLFGFTPLTSLPEKVCNPLASQVPPSRLDGPAEYAHLYQ--AIENPFL 246
DB 172 RGIIVNVVAPGFETIDMTRLSDDQAGILAOVP-AGRLGGAQEIANNVAVFLASDEAYI 230
QY 247 NGEVIRLDGALRM 259
DB 231 TGETLHVNGMYM 243
RESULT 17
5512669-4
Patent No. 5512669
APPLICANT: PEOPLES, OLIVER P.; SINSKEY, ANTHONY J.
TITLE OF INVENTION: GENE ENCODING BACTERIAL ACETOACETYL-COA
REDUCTASE
NUMBER OF SEQUENCES: 7
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,667
FILING DATE: 25-Aug-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 124,570
FILING DATE: 20-SEP-1993
APPLICATION NUMBER: 944,488
FILING DATE: 03-NOV-1992
APPLICATION NUMBER: 566,535

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[illegible]

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Db          292 FLAISPASVITGQAFITDGI 313

RESULT 12
5229279-7
; Patent No. 5229279
; APPLICANT: PEOPLES, OLIVER P.; SINSKEY, ANTHONY J.
; TITLE OF INVENTION: METHOD FOR PRODUCING NOVEL POLYESTER
; BIOPOLYMERS
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/556,535
; FILING DATE: 13-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 67,695
; FILING DATE: 29-AUG-1987
; SEQ ID NO.: 7
; LENGTH: 246
5229279-7

Query Match      22.08; Score 287.5; DB 6; Length 246;
Best Local Similarity 31.98; Pred. No. 6e-24;
Matches 81; Conservative 45; Mismatches 109; Indels 19; Gaps 7;

QY      12 VAVITGASGIGLTAERLVGOGASAVILDLPSGSE---AQAKKIGNNCVFAPADYTS 67
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      5 IAVYTGGMGGIGRAICQRLAKDGFRRVAGCGPSPRRKKLEQOKLALGFDFIASGNVAD 64
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      68 EKDVQTLALAKGFEFGVDYAVNCAGIAYASKTYNLKKGQFHTLEDPQGVLDVNLGPFN 127
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      65 WDSKTIAPDKYKSEVGEVDVLIINNAGI---TRDYERK---MTRADMDAVIDNTLISLFN 118
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      128 VIRLVAGEMGONEPDGOGRGVLIINTASVAEFGQVGOAAYSASKGIVGKTLPIARDIA 187
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      119 VTKGVIDGMA---DRGW--GRIVNISSVNGCKGFGQGTNYSPAKAGLIGFTMALAOEYA 172
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      188 PIGRWMTIAPGLTGFELTSLDEPKYCNFLASQVPPSPRLGDPAEFAHIVQAIT--ENPF 245
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      173 TKGTVNTVSGVYATIDMKAKIRQDVLDKIVATIPV-KRLGLPQLFIASICANLSESESGF 231
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      246 LNEGVIRLDGAIRM 259
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      232 STGADFSLNGILHM 245
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
US-08-375-962B-13
; Sequence 13, Application US/08375962B
; Patent No. 5731195
; GENERAL INFORMATION:
; APPLICANT: SIMON, ANDRAS; HELLMAN, Ulf; WERNSTEDT,
; APPLICANT: CHRISTER, ERIKSSON, ULF.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecule
; TITLE OF INVENTION: Which Codes for A 32 kDa Protein Having 11-CIS Retinol
; TITLE OF INVENTION: Dehydrogenase Activity, and Which Associates With P63
; TITLE OF INVENTION: a Portion of a Retinol Binding Protein Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect (Ascii standard)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/375,962B
; FILING DATE: 20-January-1995
; CLASSIFICATION: 435

```


Thu Jun 26 06:55:11 2003

us-09-931-186-8.ra1

Page 4

ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVE. N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,856A
FILING DATE: 15-MAY-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 05463-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1517
TELEFAX: (202) 887-0763
TELEX: 706141
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-440-856A-4

Query Match 22.9%; Score 299.5; DB 1; Length 333;
Best Local Similarity 32.5%; Pred. No. 4.4e-25;
Matches 92; Conservative 46; Mismatches 106; Indels 39; Gaps 5;

QY 6 RSVGLVAVITGGASGLATAEELVVGOGASAVLLDIPNSGGEQAQKLGNNCYFAPADY 65
DB 50 KRLGKVAIVTGGARGIGELVRLVKGARVVIADIDDAAGELAAALPHEGVFVCDY 109
QY 66 TSEKDVOTALAKGKFRVAVNACAGIAVASKTYNLKQQTHTLDFQVLDVNLGTT 125
DB 110 SVEEDVERAVRAVARGRDLVLCNNAGV-LGRQTRAKSTLSPDAGEPRVLEKVNALGA 168
QY 126 FNVIRLVAGKQDEPDGQGVYINTASVAAEQVGOAASASGAGIYKATLPARD 185
DB 169 ALGKHAALMTOR-----RAGSIISVASYAVGLGIPRAYASHAIVGLTKNACE 222
QY 186 LAPGIRMTAPGLFGLPL-----TSLP-----EKVC 214
DB 223 LGAGIRVNCISPPGVATPKMINAMRGHDASTADADADIDDIATVPSQEVYKMEVY 282
QY 215 NFLASQVFPRLDPAEVAHLYOATIEPNPLNGEVIRLDGAI 257
DB 283 RGLATLKGATLRPRDIAE-AALFLASDSDSRYSIASHNLVYDGVY 324

RESULT 7

US-08-815-225-4

; Sequence 4, Application US/08815225

; Patent No. 6268479

; GENERAL INFORMATION:

; APPLICANT: Stern, David M.

; TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE

; TITLE OF INVENTION: BINDING (EPAB) POLYPEPTIDE AND METHODS FOR INHIBITING

; TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESSES:

; ADDRESS: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: U.S.A.

ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,225
FILING DATE: 12-MAR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/55209
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-815-225-4

Query Match 22.8%; Score 299; DB 4; Length 255;
Best Local Similarity 33.6%; Pred. No. 3.3e-25;
Matches 85; Conservative 47; Mismatches 101; Indels 20; Gaps 8;

QY 8 VKGLVAVITGGASGLATAEELVVGOGASAVLLDIPNSGGEQAQKLGNNCYFAPADY 67
DB 4 LSKRTVITGGARGIGELVRLVKGARVVIADIDDAAGELAAALPHEGVFVCDY 109
QY 68 EKVQOTALAKGKFRVAVNACAGIAVASKTYNLKQQTHTLDFQVLDVNLGTT 127
DB 64 EEDMORVAVAREFESVGLVNNAGISTGMFL-----ETSEVERFRVVDINLTGVT 117
QY 128 VIRLVAGKQDEPDGQGVYINTASVAAEQVGOAASASGAGIYKATLPARD 187
DB 118 GKTIVPAM---KXAGG--GSIVNISAAAGLALTSYSGSKWGVGLSKLAVELG 171
QY 188 PIGIRMTAPGLFGLPL--TSLPEKVCNPLASQVFPFSRIG-DPAEVAHLYOATIE-- 242
DB 172 TDRIKRVNSVHPGMYTPMATEGIRGEGSY--PNTPM-GRVGENEGETAGAVVKILSDT 228
QY 243 NPFLNGEVIRLDG 255
DB 229 SSVYTGAEIAYDG 241

RESULT 8

US-09-134-001C-4512

; Sequence 4512, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; PRIOR FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 4512

; LENGTH: 263

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-4512

;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
;; FILE REFERENCE: 25865-1651
;; CURRENT APPLICATION NUMBER: US/09/347, 878C
;; CURRENT FILING DATE: 1999-07-06
;; NUMBER OF SEQ ID NOS: 75
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 50
;; LENGTH: 261
;; TYPE: PR1
;; ORGANISM: Homo sapiens
US-09-347-878-50

Query Match 100.0%; Score 1309; DB 4; Length 261;
Best Local Similarity 100.0%; Pred. No. 7e-138;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACRSVKGLVAVITGASGLGATTAERLVGGASAVLLDLPNSGGEAOKKLNKCVF 60
DB 1 MAACRSVKGLVAVITGASGLGATTAERLVGGASAVLLDLPNSGGEAOKKLNKCVF 60
QY 61 APADVTSEKDVOTLALAKKFGFVAVAVACAGIAVASKTYNLKKGOTHTLEDFQFVLDV 120
DB 61 APADVTSEKDVOTLALAKKFGFVAVAVACAGIAVASKTYNLKKGOTHTLEDFQFVLDV 120
QY 121 NLKGTENVIRLVAGEMQNEPDGQGRVITNTASVAAFEGOVGAAYASAKSGIVGML 180
DB 121 NLKGTENVIRLVAGEMQNEPDGQGRVITNTASVAAFEGOVGAAYASAKSGIVGML 180
QY 181 PIARDLAPIGIRWTAPLGFPLTSLPEKVCNPLASQVPPSLRGPDAEYAHVQAI 240
DB 181 PIARDLAPIGIRWTAPLGFPLTSLPEKVCNPLASQVPPSLRGPDAEYAHVQAI 240
QY 241 IENPFLNGEVIIRLDGAIRMOP 261
DB 241 IENPFLNGEVIIRLDGAIRMOP 261

RESULT 4
US-08-980-832-41
;; Sequence 41, Application US/08980832B
;; Patent No. 6291204
;; GENERAL INFORMATION:
;; APPLICANT: Pasamontes, Luis
;; APPLICANT: Tsygankov, Yuri
;; TITLE OF INVENTION: Improved Fermentative Carotenoid Production
;; FILE REFERENCE: Improved Fermentative Carotenoid
;; CURRENT APPLICATION NUMBER: US/08/980, 832B
;; CURRENT FILING DATE: 1997-12-01
;; NUMBER OF SEQ ID NOS: 66
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 41
;; LENGTH: 388
;; TYPE: PR1
;; ORGANISM: Flavobacterium sp. R1534
US-08-980-832-41

Query Match 50.8%; Score 664.5; DB 4; Length 388;
Best Local Similarity 55.5%; Pred. No. 1.1e-65;
Matches 141; Conservative 35; Mismatches 69; Indels 9; Gaps 3;

QY 8 VKGLVAVITGASGLGATTAERLVGGASAVLLDLPNSGGEAOKKLNKCVFAPADVT 67
DB 143 IEGRVAVVTTGAASGLGASAMLAQGAQVVLADL-----AEKDAPEGAVHAAQVTD 196
QY 68 EKDVTALALAKKFGFVAVAVACAGIAVASKTYNLKKGOTHTLEDFQFVLDVNLKGT 127
DB 197 ATAQGTALALATDFGRDLGVAVACAGIAVASKTYNLKKGOTHTLEDFQFVLDVNLKGT 254
QY 128 VIRLVAGEMQNEPDGQGRVITNTASVAAFEGOVGAAYASAKSGIVGMLPIARDLA 187
DB 255 MARLAAMARNEPVR--GERGVIVNTASIAAQDQIQVAVYAAASKAGVAGWTLPARDLA 313
188 PICTRYMTIANGTGTETITSI PRKYCNPLASQVPPSPRI GDPAFVAVHIVQATTFENFTN 247

DB 314 RHGIRVMTIANGTGTETITSI PRKYCNPLASQVPPSPRI GDPAFVAVHIVQATTFENFTN 247
QY 248 GEVIRLDGAIRMOP 261
DB 374 GEVIRLDGAIRMOP 387

RESULT 5
US-09-239-052-2
;; Sequence 2, Application US/09239052
;; Patent No. 6346395
;; GENERAL INFORMATION:
;; APPLICANT: Holmes, David J.
;; APPLICANT: Zhong, Yiyi
;; APPLICANT: Debouck, Christine
;; APPLICANT: Jaworski, Deborah D.
;; APPLICANT: Wang, Min
;; APPLICANT: Warren, Richard L.
;; APPLICANT: Kosmatka, Anna L.
;; APPLICANT: McDevitt, Damien
;; APPLICANT: Ingraham, Karen A.
;; APPLICANT: Chalke, Alison F.
;; APPLICANT: So, Chi Young
;; APPLICANT: Wallis, Nicola G.
;; APPLICANT: Pearson, Stewart C.
;; TITLE OF INVENTION: FdG
;; FILE REFERENCE: GM10191
;; CURRENT APPLICATION NUMBER: US/09/239, 052
;; CURRENT FILING DATE: 1999-01-27
;; NUMBER OF SEQ ID NOS: 2
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO: 2
;; LENGTH: 243
;; TYPE: PR1
;; ORGANISM: Streptococcus pneumoniae
US-09-239-052-2

Query Match 24.9%; Score 326.5; DB 4; Length 243;
Best Local Similarity 35.1%; Pred. No. 2.6e-28;
Matches 88; Conservative 56; Mismatches 104; Indels 23; Gaps 6;

QY 15 ITGASGLGATTAERLVGGASAVLLDLPNSGGE-----AOAKKLNKCVFAPADVTSE 68
DB 10 ITGSSKIGLALAHKRAQGANIVL-----NSRGAISELLAFSNVGIKRVFISGDVDF 65
QY 69 KDVOTLALAKKFGFVAVAVACAGIAVASKTYNLKKGOTHTLEDFQFVLDVNLKGT 128
DB 66 ADKRMIDQALIELGVDVAVNAGI--TQDTLMK-----TEAPEKLVNLGAEFM 119
QY 129 IRLVAGEMQNEPDGQGRVITNTASVAAFEGOVGAAYASAKSGIVGMLPIARDLA 188
DB 120 TQSVL-----KPMKARAGATINNSVGLMGNIGQANYAASKGLIGFTSVAREVAS 173
QY 189 IGRVMTIANGTGTETITSI PRKYCNPLASQVPPSPRI GDPAFVAVHIVQATTFENFTN 247
DB 174 RNRVAVIAPGIESDMTALISDKIKETLAQIPM--KEFGAEOVAVDLTVFLAGODVLTG 232
QY 249 EVIRLDGAIRMOP 259
DB 233 QVTAIDGGLSM 243

RESULT 6
US-08-440-856A-4
;; Sequence 4, Application US/08440856A
;; Patent No. 5750873
;; GENERAL INFORMATION:
;; APPLICANT: DELAPORTA, STEPHEN L.
;; TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
;; NUMBER OF SEQUENCES: 9
;; CORRESPONDENCE ADDRESSES:

ALIGNMENTS

RESULT 1

US-08-815-225-2

; Sequence 2, Application US/08815225

; Patent No. 6268479

; GENERAL INFORMATION:

; APPLICANT: Stern, David M.

; APPLICANT: Yan, Shi Du

; TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE

; TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING

; TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: U.S.A.

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/815,225

; FILING DATE: 12-MAR-1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 0575/55209

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 278-0400

; TELEFAX: (212) 391-0525

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 261 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-815-225-2

Query Match 100.0%; Score 1309; DB 4; Length 261;

Best Local Similarity 100.0%; Pred. No. 7e-138;

Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MAAACRSYKGLVAVITGGASGLGATAEKLVGOGASAVLLDLPNSGGEAQAQKLNQCVF 60
OY 61 APADVTSEKDVQOTALALAKGKFRVDVAVNCAGIAVASKTYNKKGGTHLEDFORVLDV 120
DB 61 APADVTSEKDVQOTALALAKGKFRVDVAVNCAGIAVASKTYNKKGGTHLEDFORVLDV 120
OY 121 NLMGTFNVIRLVAGEMGNEPDGOGRGVINTASVAAFEGOVGOAAYSASKGIVGML 180
DB 121 NLMGTFNVIRLVAGEMGNEPDGOGRGVINTASVAAFEGOVGOAAYSASKGIVGML 180
OY 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKVCNFIASQVFPFSLGDPAEYAHLYQAI 240
DB 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKVCNFIASQVFPFSLGDPAEYAHLYQAI 240
OY 241 IENPFLNGEYIRLDGAIKMP 261
DB 241 IENPFLNGEYIRLDGAIKMP 261
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RESULT 2

US-08-815-225-3

; Sequence 3, Application US/08815225

; Patent No. 6268479

; GENERAL INFORMATION:

; APPLICANT: Stern, David M.

; APPLICANT: Yan, Shi Du

; TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE

; TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING

; TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: U.S.A.

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/815,225

; FILING DATE: 12-MAR-1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 0575/55209

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 278-0400

; TELEFAX: (212) 391-0525

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 261 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-815-225-3

Query Match 100.0%; Score 1309; DB 4; Length 261;

Best Local Similarity 100.0%; Pred. No. 7e-138;

Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MAAACRSYKGLVAVITGGASGLGATAEKLVGOGASAVLLDLPNSGGEAQAQKLNQCVF 60
DB 1 MAAACRSYKGLVAVITGGASGLGATAEKLVGOGASAVLLDLPNSGGEAQAQKLNQCVF 60
OY 61 APADVTSEKDVQOTALALAKGKFRVDVAVNCAGIAVASKTYNKKGGTHLEDFORVLDV 120
DB 61 APADVTSEKDVQOTALALAKGKFRVDVAVNCAGIAVASKTYNKKGGTHLEDFORVLDV 120
OY 121 NLMGTFNVIRLVAGEMGNEPDGOGRGVINTASVAAFEGOVGOAAYSASKGIVGML 180
DB 121 NLMGTFNVIRLVAGEMGNEPDGOGRGVINTASVAAFEGOVGOAAYSASKGIVGML 180
OY 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKVCNFIASQVFPFSLGDPAEYAHLYQAI 240
DB 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKVCNFIASQVFPFSLGDPAEYAHLYQAI 240
OY 241 IENPFLNGEYIRLDGAIKMP 261
DB 241 IENPFLNGEYIRLDGAIKMP 261
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RESULT 3

US-09-347-878-50

; Sequence 50, Application US/09347878C

; Patent No. 6376210

; GENERAL INFORMATION:

; APPLICANT: Yuan, Chong

Thu Jun 26 06:55:11 2003

us-09-931-186-8.rai

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:24:27 ; Search time 12.1667 Seconds

(without alignments)
631.182 Million cell updates/sec

Title: US-09-931-186-8
Perfect score: 1309
Sequence: 1 MAACRSVKGLAVITGAS.....ENPLNGEIVRLDQAIKMP 261

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents_Aa.*
1: /cgn2.6/ptodata/1/1aa/5A.CONB.pep.*
2: /cgn2.6/ptodata/1/1aa/5B.CONB.pep.*
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4: /cgn2.6/ptodata/1/1aa/6B.CONB.pep.*
5: /cgn2.6/ptodata/1/1aa/PCRTOS.CONB.pep.*
6: /cgn2.6/ptodata/1/1aa/backfilest.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1309	100.0	261	4	US-08-815-225-2
2	1309	100.0	261	4	US-08-815-225-3
3	1309	100.0	261	4	US-08-815-225-4
4	664.5	50.8	388	4	US-08-980-832-41
5	326.5	24.9	243	4	US-09-239-052-2
6	299.5	22.9	333	1	US-08-440-856A-4
7	299	22.8	255	4	US-08-815-225-4
8	295	22.5	263	4	US-09-134-001C-4512
9	292.5	22.3	262	4	US-09-363-189B-6
10	291	22.2	315	3	US-08-793-035-9
11	291	22.2	315	3	US-08-793-035-10
12	287.5	22.0	246	6	5229279-7
13	285.5	21.8	244	1	US-08-375-962B-13
14	285.5	21.8	244	1	US-08-562-114B-13
15	285.5	21.8	244	4	US-08-729-594A-13
16	285.5	21.8	244	4	US-08-937-993-13
17	282.5	21.6	273	6	5512659-4
18	278.5	21.3	274	4	US-09-134-001C-4431
19	273.5	20.9	249	4	US-09-134-001C-4825
20	269.5	20.6	246	3	US-09-238-481-2
21	269.5	20.6	246	3	US-09-572-810A-2
22	269	20.6	231	4	US-09-134-001C-4397
23	268	20.5	186	4	US-08-858-207A-370
24	267.5	20.4	337	1	US-08-440-856A-3
25	266	20.3	256	4	US-09-504-358-14
26	266	20.3	256	4	US-09-954-314-14
27	264	20.2	247	1	US-08-241-766-13

28	255.5	19.5	263	6	5229279-4	Patent No. 5229279
29	254	19.4	261	4	US-09-468-738A-29	Sequence 29, Appl
30	254	19.4	261	4	US-09-940-019-29	Sequence 29, Appl
31	252.5	19.3	257	4	US-09-134-001C-3562	Sequence 3562, Ap
32	252.5	19.3	253	4	US-09-134-001C-3505	Sequence 3505, Ap
33	249.5	19.1	222	3	US-08-822-322-8	Sequence 8, Appl
34	249.5	19.1	222	3	US-09-666-109-8	Sequence 8, Appl
35	245	18.7	256	1	US-08-594-808B-7	Sequence 7, Appl
36	243	18.6	271	2	US-07-637-865-2	Sequence 2, Appl
37	242	18.5	359	1	US-08-440-856A-8	Sequence 8, Appl
38	238	18.2	258	4	US-09-504-358-12	Sequence 12, Appl
39	238	18.2	258	4	US-09-054-314-12	Sequence 12, Appl
40	238	18.2	222	3	US-09-109-205-2	Sequence 2, Appl
41	238	18.2	222	3	US-09-443-184-58	Sequence 58, Appl
42	228.5	17.5	251	3	US-08-822-322-9	Sequence 9, Appl
43	228.5	17.5	251	3	US-09-466-109-9	Sequence 9, Appl
44	223	17.0	283	4	US-09-367-012-1	Sequence 1, Appl
45	223	17.0	283	4	US-09-777-157A-1	Sequence 1, Appl
46	214	16.3	267	4	US-09-134-001C-5042	Sequence 5042, Ap
47	211	16.1	283	4	US-09-134-001C-5346	Sequence 5346, Ap
48	206	15.7	250	4	US-09-134-001C-4339	Sequence 4339, Ap
49	206	15.7	313	4	US-09-413-814-9	Sequence 9, Appl
50	204	15.6	244	2	US-09-090-567-2	Sequence 2, Appl
51	189	14.4	248	4	US-09-385-028-11	Sequence 11, Appl
52	185.5	14.2	295	3	US-09-002-298-5	Sequence 5, Appl
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58	184.5	14.1	318	4	US-08-937-993-39	Sequence 39, Appl
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61	182.5	13.9	295	4	US-09-134-001C-4059	Sequence 4059, Ap
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QY 121 NMGTENVIRLVAGEMQNEPDGQGVIIINTASVAAPFGVGOQAAYSASKGIYGMTL 180
DB 114 NLGTVTLTKLALPYLRKSQ-----GNVINISLVGAIGQAVPYVATKGAVTAMTK 166
QY 181 PIANDLAPICIRVTTIPGLFGPTLTLSPKXCNPLASGVPPP-----SRL 227
DB 167 ALALDESPYGVRCNSCISINWIPLMEE-----LAALPDPFRATIREGMLAQLGRM 218
QY 228 GDPAEV-AHLVQAIENPFLNG-EVIRLDGA 256
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Query Match 22.28; Score 290.5; DB 9; Length 270;
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GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsens, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PTC9
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PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 22.2%; Score 290.5; DB 9; Length 270;
Best Local Similarity 31.7%; Pred.No. 1.3e-18;
Matches 86; Conservative 42; Mismatches 106; Indels 37; Gaps 8;

QY 1 MAACRSYKGLVAVITGGASGLATARTLVGGASAVILDLPPNSGGPAAKXKLNOCVF 60
DB 1 MATGTR-YAGKVVYGGGRIAGIVRAEVNSGARVYICDKDSGGALAEQL-PCAVF 58
QY 61 APADYTSKEDYQOTALALAKRGFRVYVNCAGIAVASKTYNLKKGQTHLEDFQVLDV 120
DB 59 ILCDVTQEDVDYKTLVSETIRRGRLDCVNNAGHHPD-----QRPETSAGCFRLEL 113
QY 121 NLMGTFNVIIRLVASGMGNEPDGQGRVYIINTASVAFBGOVGAASAKGIVGTL 180
DB 114 NLGTYTTLKIALPYLRKSQ-----GNVINTSSLVGALQQAQVPIVATKGAVTATK 166
QY 181 PIARDLAPIGRVMTIAPGLTGTPLTSLPERVCNFIASQVFP-----SRL 227
DB 167 ALALDESPIYGVNVNIGSNITWPLME-----LALMDPFRATIREGLAQPIGRM 218
QY 228 GPDAEY-AHLVQATIEENPLNG-EYIRLDGA 256
DB 219 GQPAEYGAAYFLASEANCITGIELLVYGA 249

RESULT 24
US-09-978-697-468
Sequence 468, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoul, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697

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; ORGANISM: Gluconobacter oxydans
; US-09-802-853-6
Query Match      22.3%  Score 292.5; DB 10; Length 262;
Best Local Similarity 31.6%; Pred. No. 8.3e-19;
Matches 86; Conservative 41; Mismatches 110; Indels 35; Gaps 7;

QY 6 RSVAGLVAVITGASGLATAEERLVGASAVLLDPNSG---GENAARKLGNMCFAP 62
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 3 KKEFGKVLTVGAGGNIGIALRLAEGETAIALDDNREALEKAEVSEKVEARASY 62
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 63 ADVTSEADVQATALAKGKGRVAVNACGIAVASTYMLKQQTHTLEDFOEVLVNL 122
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 63 CDVTSERAVIGTVSVVVDGEKIDFLNNAGYOGA---FAPYQDPSDDFAFVLTINV 117
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 123 MGTENVIRLVAGEM-GONEPDOGSGRGVIINTASVAFAEGOVGOAASASKGIVGNTLP 181
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 118 TGAFHVLKAVSRQMTQN-----YGRIVNTASMAGVKPPNMAAGASRGATIALTER 170
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 182 IARLAPLIGIRVMTIAPGLF-----GTPLTSLPEKVCNPLASQVPPPS 225
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 171 AALDLAPNIRVNAISGTYMGPFMREROVELAKVGSQYFSTDPKVVAQOMIGSVPM-R 229
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 226 RLGDPAEYAHVQAII--ENPFLNGEVIRLDG 255
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 230 RYGDINELPQVVAFLGDSDSFMGTGVNLPING 261
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 23
US-09-978-295A-468
; Sequence 468, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978-295A
; PRIOR APPLICATION NUMBER: 2001-10-15
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
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; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
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;; TYPE: PRT
;; ORGANISM: Bacillus megaterium
US-09-479-040-9

Query Match 23.0%; Score 301; DB 9; Length 247;
Best Local Similarity 29.1%; Pred. No. 1,3e-19;
Matches 78; Conservative 59; Mismatches 93; Indels 38; Gaps 9;

QY 7 SVKGLVAVITGASGLTAEERLYVGG-----ASAVLLDLPNSGGEQAK 53
DB 3 TLQKRVAVITGSGSGLATRELASNGVAVANNYSKSSAKAIKELDNGEA-----58
QY 54 LGNNCPAPADVTSEKDVOTALAKGKFRVDVAVNACIAVASKTYNLK-GQTHLE 112
DB 59 -----IAVQADVSVYDQAKHLIEETKAFGLDILVNNAGI---TRDRSFKLGE-----E 106
QY 113 DFOKVLVNMKGTNNVRLVAGENGQNEPDGQRGVITNTASVAEFGVQGAAYSASK 172
DB 107 DMKRVIDVNLHSVNTTSALTLESE---GGR---VINISITGAGSGFGQTNISAK 160
QY 173 GGIYMTLPARDLAPIGIRVMTIAPGLFGLPLTSLPERVCNPLASQVFPFRLGDPAP 232
DB 161 AGMGLPKSLALELAKGVTVNAICPGFIETEMVAIPEDVAKIYAKIP-TRRLGAAE 219
QY 233 YAH-LVQAIENPFLNGEVRIDGAIKM 259
DB 220 IARGVYLAKDGAITGQOLNINGLYM 247

RESULT 20

US-09-773-748-1
; Sequence 1, Application US/09773748
; Publication No. US20020187537A1
; GENERAL INFORMATION:
; APPLICANT: Masaru
; TITLE OF INVENTION: Levodione reductase gene and use thereof
; FILE REFERENCE: Levodione reductase
; CURRENT APPLICATION NUMBER: US/09/773,748
; CURRENT FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: EP00101665.8
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Corynebacterium aquaticum
US-09-773-748-1

Query Match 22.4%; Score 293.5; DB 9; Length 267;
Best Local Similarity 31.8%; Pred. No. 6.9e-19;
Matches 84; Conservative 45; Mismatches 98; Indels 37; Gaps 9;

QY 12 VAVITGASGLTAEERLYVGGASAVLLDLPNSGGEQAKKIGNCCVAF-----ADVT 66
DB 15 VVLTGGSGGLGRATRAVRLAELSLVDVSSGLESKAAVLETPADAEVLTVDVS 74
QY 67 SEKDVOITALALAKGKFRVDVAVNACIAVASKTYNLKQTHLEDFQRLVDVNMKGT 126
DB 75 DEAGVEAVYATTEHFGSLIDGFENNAIEGKQ-----NPTSFTAAEDKYVSIIRGVF 129
QY 127 ----NVITLVAGEMQNEPDGQRGVITNTASVAEFGVQGAAYSASKGIGYMTLP 182
DB 130 LGLEKYLKIMR-----EAGS--GMVYNTASVGGIRGIGNSGYAAAKRGVGLRNS 179
QY 183 AADLAPIGIRVMTIAPGLFGLPLTSL-----PERVCNPLASQVFPFRLGDPAP 233
DB 180 AVEYGRYGRIRMAIPGALWPMVNSKQJDPENRRAAEFI--QVNPCKRGEAPEI 237
QY 234 AHLVQAIENPFLNGEVRIDG 255
DB 238 AAVVAFLSDDASVYNAATVPIDG 261

RESULT 21
US-10-307-385-6
; Sequence 6, Application US/10307385
; Publication No. US2003007797A1
; GENERAL INFORMATION:
; APPLICANT: SUGIYAMA, MASAKAZU
; APPLICANT: TONOUCHI, NAOTO
; APPLICANT: SUZUKI, SHUNICHI
; APPLICANT: YOKOZAKI, KENZO
; TITLE OF INVENTION: XYLILOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF
; FILE REFERENCE: 0010-1024-0
; CURRENT APPLICATION NUMBER: US/10/307,385
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US/09/363,189
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: JP10-216047
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Gluconobacter oxydans
US-10-307-385-6

Query Match 22.3%; Score 292.5; DB 9; Length 262;
Best Local Similarity 31.6%; Pred. No. 8.3e-19;
Matches 86; Conservative 41; Mismatches 110; Indels 35; Gaps 7;

QY 6 RSVKGLVAVITGASGLTAEERLYVGGASAVLLDLPNSG---GEQAKKIGNCCVAF 62
DB 3 KRFNGKVCVLTGAGNIGLALRLAEBGATLALDMNRELEKASVREKGEARSV 62
QY 63 ADVTSEKDVOTALALAKGKFRVDVAVNACIAVASKTYNLKQTHLEDFQRLVDVL 122
DB 63 CDVTSEAVYIGTVDSVRDFGKIDFLNNAGVGA-----FAPVQDPSPDDFAVLTIV 117
QY 123 MGTENVIRLVAGEM-QONEPDGQRGVITNTASVAEFGVQGAAYSASKGIGYMTLP 181
DB 118 TGAHYLKAASRMION-----YGRVTNLSAGVAGPMMAYGASKGAILIATBT 170
QY 182 IARDLAPIGIRVMTIAPGLF-----GTPILSLPERVCNPLASQVFPF 225
DB 171 AADLAPYINRVAIISPGVGPFWMERQVELOAKVSOYFTDPKVAQOMIGVPM-R 229
QY 226 RLGDPAEYAHVQAI--ENPFLNGEVRIDG 255
DB 230 RYGDINIRPGVAVFLIGDSSFTMTGVNLPFAG 261

RESULT 22
US-09-802-853-6
; Sequence 6, Application US/09802853
; Patent No. US20010034049A1
; GENERAL INFORMATION:
; APPLICANT: SUGIYAMA, MASAKAZU
; APPLICANT: TONOUCHI, NAOTO
; APPLICANT: SUZUKI, SHUNICHI
; APPLICANT: YOKOZAKI, KENZO
; TITLE OF INVENTION: XYLILOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF
; FILE REFERENCE: 0010-1024-0
; CURRENT APPLICATION NUMBER: US/09/802,853
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 09/363,189
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP10-216047
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 262
; TYPE: PRT

QY 12 VAVITGASGLTAEERLYVGGASAVLLDLPNSGGEQAKKIGNCCVAF-----ADVT 66
DB 15 VVLTGGSGGLGRATRAVRLAELSLVDVSSGLESKAAVLETPADAEVLTVDVS 74
QY 67 SEKDVOITALALAKGKFRVDVAVNACIAVASKTYNLKQTHLEDFQRLVDVNMKGT 126
DB 75 DEAGVEAVYATTEHFGSLIDGFENNAIEGKQ-----NPTSFTAAEDKYVSIIRGVF 129
QY 127 ----NVITLVAGEMQNEPDGQRGVITNTASVAEFGVQGAAYSASKGIGYMTLP 182
DB 130 LGLEKYLKIMR-----EAGS--GMVYNTASVGGIRGIGNSGYAAAKRGVGLRNS 179
QY 183 AADLAPIGIRVMTIAPGLFGLPLTSL-----PERVCNPLASQVFPFRLGDPAP 233
DB 180 AVEYGRYGRIRMAIPGALWPMVNSKQJDPENRRAAEFI--QVNPCKRGEAPEI 237
QY 234 AHLVQAIENPFLNGEVRIDG 255
DB 238 AAVVAFLSDDASVYNAATVPIDG 261

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; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257, 931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269, 308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13581
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13581
```

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Query Match          24.9%; Score 326.5; DB 10; Length 243;
Best Local Similarity 35.1%; Pred. No. 6.2e-22;
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;
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QY 15 ITGASGLGATAEELVQASAVLLDLPNSGE-----AQAKLGNVCYFAPADYTS 68
    ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 10 ITGSRGIGLAIAHFAQAGANIVL---NSRGAISELLAEFSNGYKRVPIGSDVDF 65
QY 69 KDVALALAKGKFRVAVAVANCAGIAVASKTYNLKKGQTHLEDFQVLDVNLMTGFNV 128
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 66 ADAKRMIDQALAEISVYLVNNGI---TQPTLMKM-----TEADFEKVLKVNLTGAFNM 119
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 129 IRLVAGENGQNEPDGGGQGVYIINTASVAFAEGQVQAAYASAKGIVGWTLPARDLAP 188
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 120 TQSVL-----KPMKAKAREGAIINMSYVGLMGNGQANVYASAKGLIGFTKSVAREVAS 173
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 189 IGIKMTIAPGLFPLLTSLPEKYCNFLASQVPPSRGDPAEYAHVQALITENPLNG 248
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 174 RNIRNVNAPGHTESDMRAILSDRIKELTQAQIPK-KFQGAQEDVADLTIVLAQGDYLTG 232
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 EVIRLDGALRM 259
    : || : || : || : || : || : || : || : || : || : || : || : ||
DB 233 GYVIAIDGGLSM 243
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```

RESULT 15
US-09-815-242-10921
; Sequence 10921, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Cair, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA 011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10921
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; LENGTH: 245
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10921
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```

Query Match          24.3%; Score 318.5; DB 10; Length 245;
Best Local Similarity 33.7%; Pred. No. 3.3e-21;
Matches 84; Conservative 38; Mismatches 108; Indels 19; Gaps 5;
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```

QY 15 ITGASGLGATAEELVQASAVLLD---LPNSGGEQAQAKLGNVCYFAPADYTSERD 70
    ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 10 ITGSTRGIGKAVALAKKAGANIVLNGRSEITPEQROEIEA--FVKICIGLSGDISDPA 67
QY 71 VQTALALAKGKFRVAVAVANCAGIAVASKTYNLKKGQTHLEDFQVLDVNLMTGFNVIR 130
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 68 AGEMIQATVDQLGSIDILVNNAGIT-----NDKLLRMTKEDFNACLDINLVGFNMQ 121
QY 131 LVAGENGQNEPDGGGQGVYIINTASVAFAEGQVQAAYASAKGIVGWTLPARDLAP 190
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 122 QAVKRMKQ-----KSGRIINMASYVGLMGNGQANVYASAKGIVGFTKSVAREVAPRG 175
QY 191 IRVMTIAPGLFPLLTSLPEKYCNFLASQVPPSRGDPAEYAHVQALITENPLNGVY 250
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 176 ITCNALAPGFIQTEMIDVLESEKVTQMNQIPLOT-FGQVEDVAAVAFILAKSPYITGOV 234
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 251 IRLDGLARM 259
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DB 235 VNVDDGLVM 243
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```

RESULT 16
US-10-175-696-14
; Sequence 14, Application US/10175696
; Publication No. US20030092658A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Meyers, Rachel
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-193001
; CURRENT APPLICATION NUMBER: US/10/175,696
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 10/067,668
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/266,140
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/823,901
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US01/10720
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/193,920
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/862,658
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PCT/US01/16380
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/205,675
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/882,837
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: PCT/US01/19319
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/211,727
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-175-696-14
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Query Match          24.0%; Score 314; DB 9; Length 237;
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```
/ Patent No. US20020132319A1
/ GENERAL INFORMATION:
/ APPLICANT: ABERO, MELWYN A.
/ APPLICANT: AGREE, CHARLES S.
/ APPLICANT: AUST, ROBERT
/ APPLICANT: KISSINGER, CHARLES R.
/ APPLICANT: MARGOSIAR, STEVE
/ APPLICANT: MENG, JERRY J.
/ APPLICANT: PELLETIER, LAURA A.
/ APPLICANT: REJTO, PAUL A.
/ APPLICANT: SHOWALTER, RICHARD E.
/ APPLICANT: TEMPCZYK-RUSSELL, ANNA
/ APPLICANT: THOMSON, JIM
/ APPLICANT: VANDERPOOL, DARIN
/ APPLICANT: VILAFRANCA, J. ERNEST
/ TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
/ TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
/ TITLE OF INVENTION: OF INHIBITORS THEREOF
/ FILE REFERENCE: 0125-0049
/ CURRENT APPLICATION NUMBER: US/09/931,186
/ CURRENT FILING DATE: 2001-08-17
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 17
/ LENGTH: 259
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-931-186-17

Query Match      25.4%; Score 332.5; DB 10; Length 259;
Best Local Similarity 31.2%; Pred. No. 1.9e-22;
Matches 83; Conservative 51; Mismatches 105; Indels 27; Gaps 7;
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QY 8 VGGVAVITGGASGLGATFAERLVQGSASAVLLDLPNSGGEAQAQKL-----GN 56
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 7 LRSALAVITGGASGLGATFAERLVQGSASAVLLDLPNSGGEAQAQKL-----GN 66
QY 57 NCVFADVTSEKDVQALALAKGFRG-VDVAVNCAGIAVASKTYNKKQOTHTLEDFQ 115
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 67 HAAF-QADVSEARARCLLEQVQACFSRPSVYVSCAIGITDEFLHMS-----DWD 119
QY 116 RVLDVNLGTFENVILVAGENGQNEPDGQGVINTASVAALFEGOVQAAVSASKGI 175
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 KYIAVNLGTFENVILVAGENGQNEPDGQGVINTASVAALFEGOVQAAVSASKGI 174
QY 176 VGMPLIARDLAPIGIRVMTIAPGLFGPPLTSLPEKVCNPLASQVPPSRLDPAEYAH 235
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 175 IGLFTQARRELGRHGRHICNSVLPGRIPMTQKQVYDKITTEIPM-GHLGDEEDVAD 233
QY 236 LVQ--AIENPRLNGEVRILGDAIRM 259
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 234 VVAFLASEDSGITGTSTVEVTGGLFM 259
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RESULT 13
US-09-815-242-13360
/ Sequence 13360, Application US/09815242
/ Patent No. US20020061569A1
/ GENERAL INFORMATION:
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari L.
/ APPLICANT: Zyskind, Judith W.
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John D.
/ APPLICANT: Carr, Grant J.
/ APPLICANT: Yamamoto, Robert T.
/ APPLICANT: Xu, H. Howard
/ TITLE OF INVENTION: Identification of Essential Genes in
/ FILE REFERENCE: ELITRA.011A
/ CURRENT APPLICATION NUMBER: US/09/815,242
/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/191,078
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/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 14110
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13360
/ LENGTH: 243
/ TYPE: PRT
/ ORGANISM: Streptococcus pneumoniae
US-09-815-242-13360
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Query Match      24.9%; Score 326.5; DB 10; Length 243;
Best Local Similarity 35.1%; Pred. No. 6.2e-22;
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;
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QY 15 ITGASGLGATFAERLVQGSASAVLLDLPNSGGEAQAQKL-----QAQKLLGNVCVAFADVTSE 68
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 10 ITGSSRGITGLAIHAKFQAQANITVL-----NSRGAISEBLLAEFSNYGIRVPISSGVSDP 65
QY 69 KDVQFALALAKGFRGVDAVAVNCAGIAVASKTYNKKQOTHTLEDFQRYLDVNLGTFENV 128
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 66 ADARFMDQAIHAKFQASDVAVNNAGI--TODTLMKV---TEADEKYLKVLGTAFNM 119
QY 129 IRLVAGMGQNEPDGQGVINTASVAALFEGOVQAAVSASKGIIVGWTLPRIARDLAP 188
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 TQSVL-----KPMKMRREGAIIINMSVGLMKNIGCANNAASKADLIGFTKVAAREVAS 173
QY 189 IGIIVMTAPGLGTFPLTSLPEKVCNPLASQVPPSRLDPAEYAHVQAIENPFLNG 248
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 174 RNIVVAVIAGMIESDMTALISDKIKETLAQIPM-KEFQAAQVADLTFTVLGQDYLNG 232
QY 249 EVIRLDGAIRM 259
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 233 QVIAIDGGLSM 243
```

```
RESULT 14
US-09-815-242-13581
/ Sequence 13581, Application US/09815242
/ Patent No. US20020061569A1
/ GENERAL INFORMATION:
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari L.
/ APPLICANT: Zyskind, Judith W.
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John D.
/ APPLICANT: Carr, Grant J.
/ APPLICANT: Yamamoto, Robert T.
/ APPLICANT: Xu, H. Howard
/ TITLE OF INVENTION: Identification of Essential Genes in
/ FILE REFERENCE: ELITRA.011A
/ CURRENT APPLICATION NUMBER: US/09/815,242
/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
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Thu Jun 26 06:55:11 2003

us-09-931-186-8. rapb

Page 6

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; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 245
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-983-966-245
Query Match      87.5%; Score 1146; DB 9; Length 227;
Best Local Similarity 100.0%; Pred. No. 2.7e-96;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      35 ASAVLLDLPNSGGEQAQKKGNNCFAPADVTSEKDVQTALALAKGKRGVAVNCAGI 94
      |||||||
DB      1 ASAVLLDLPNSGGEQAQKKGNNCFAPADVTSEKDVQTALALAKGKRGVAVNCAGI 60
      |||||||
QY      95 AVASKTYNLKKGQHTLEDFOQRLVDVNLMGTFNVIRLVAGEMGONEPDGQGRVYIINTA 154
      |||||||
DB      61 AVASKTYNLKKGQHTLEDFOQRLVDVNLMGTFNVIRLVAGEMGONEPDGQGRVYIINTA 120
      |||||||
QY      155 SVAAFEGVGOAAYASASKGIGVMTLPRIARDLAPIGIRVMTIAPGLTSLPERKVC 214
      |||||||
DB      121 SVAAFEGVGOAAYASASKGIGVMTLPRIARDLAPIGIRVMTIAPGLTSLPERKVC 180
      |||||||
QY      215 NFLASQVPPSPRLGDPAEYAHLVQAIINPFLNGEVRIRLDGAIKMP 261
      |||||||
DB      181 NFLASQVPPSPRLGDPAEYAHLVQAIINPFLNGEVRIRLDGAIKMP 227
      |||||||
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```

RESULT 10
US-10-143-090-245
; Sequence 245, Application US/10143090
; Publication No. US20030069406A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/10/143,090
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 245
; LENGTH: 227
; TYPE: PRT
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```

; ORGANISM: Homo sapiens
US-10-143-090-245
Query Match      87.5%; Score 1146; DB 9; Length 227;
Best Local Similarity 100.0%; Pred. No. 2.7e-96;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      35 ASAVLLDLPNSGGEQAQKKGNNCFAPADVTSEKDVQTALALAKGKRGVAVNCAGI 94
      |||||||
DB      1 ASAVLLDLPNSGGEQAQKKGNNCFAPADVTSEKDVQTALALAKGKRGVAVNCAGI 60
      |||||||
QY      95 AVASKTYNLKKGQHTLEDFOQRLVDVNLMGTFNVIRLVAGEMGONEPDGQGRVYIINTA 154
      |||||||
DB      61 AVASKTYNLKKGQHTLEDFOQRLVDVNLMGTFNVIRLVAGEMGONEPDGQGRVYIINTA 120
      |||||||
QY      155 SVAAFEGVGOAAYASASKGIGVMTLPRIARDLAPIGIRVMTIAPGLTSLPERKVC 214
      |||||||
DB      121 SVAAFEGVGOAAYASASKGIGVMTLPRIARDLAPIGIRVMTIAPGLTSLPERKVC 180
      |||||||
QY      215 NFLASQVPPSPRLGDPAEYAHLVQAIINPFLNGEVRIRLDGAIKMP 261
      |||||||
DB      181 NFLASQVPPSPRLGDPAEYAHLVQAIINPFLNGEVRIRLDGAIKMP 227
      |||||||
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```

Query Match      50.8%; Score 664.5; DB 9; Length 388;
Best Local Similarity 55.5%; Pred. No. 2.6e-52;
Matches 141; Conservative 35; Mismatches 69; Indels 9; Gaps 3;
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```

QY      8 VKGLVAVITGGASGIGLATIARLVGASAVLLDLPNSGGEQAQKKGNNCFAPADVT 67
      |||||||
DB      143 IEGRVFVVTGASGIGLATIARLVGASAVLLDLPNSGGEQAQKKGNNCFAPADVT 196
      |||||||
QY      68 EKVQVQALALAKGKRGVAVNCAGIYASKTYNLKKGQHTLEDFOQRLVDVNLMGTFN 127
      |||||||
DB      197 ATAAQTALADNRFRLEDGLVNCAGIAPAEK--LGRDGPGLDSFRAAVTINLIGSEN 254
      |||||||
QY      128 VIRLVAGEMGONEPDGQGRVYIINTASVAAFEGVGOAAYASASKGIGVMTLPRIARDL 187
      |||||||
DB      255 MARLAAPAMARNBPVR-GERGVYVNTASIAADQGLQGVAYASAKGAGVMTLPARDLA 313
      |||||||
QY      188 PIGIRVMTIAPGLTSLPERKVCNFLASQVPPSPRLGDPAEYAHLVQAIINPFLN 247
      |||||||
DB      314 RHGIRVMTIAPGLTSLPERKVCNFLASQVPPSPRLGDPAEYAHLVQAIINPFLN 373
      |||||||
QY      248 GEVIRLDGAIKMP 261
      |||||||
DB      374 GEVIRLDGAIKMP 387
      |||||||
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RESULT 12
US-09-931-186-17
; Sequence 17, Application US/09931186
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Db 61 AAPADVTSEEDVOTALALAKGKGRVDVAVNCAAGINAVASTYLNKKQCTHTLDDPQAVLDV 120
QY 121 NMGTENVIRLVAGENGQNEPDGGGQGVYINTASVAEFGVGQAAYASASGKGYGML 180
Db 121 NMGTENVIRLVAGENGQNEPDGGGQGVYINTASVAEFGVGQAAYASASGKGYGML 180
QY 181 PIARDLAPIGIRVMTLAPGFGFPLTSLPEKVCNPLASQVPPPSRLGDPAEYAHLYQAI 240
Db 181 PIARDLAPIGIRVMTLAPGFGFPLTSLPEKVCNPLASQVPPPSRLGDPAEYAHLYQAI 240
QY 241 IENPFLNGEVIRLDGAIKMQP 261
Db 241 IENPFLNGEVIRLDGAIKMQP 261
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RESULT 6

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US-09-931-186-2
; Sequence 2, Application US/09931186
; Patent No. US20020132319A1
; GENERAL INFORMATION:
; APPLICANT: ABREO, MELWYN A.
; APPLICANT: AGREE, CHARLES S.
; APPLICANT: AUST, ROBERT
; APPLICANT: KISSINGER, CHARLES R.
; APPLICANT: MARGOSIAK, STEVE
; APPLICANT: MENZ, JERRY J.
; APPLICANT: PELLETIER, LAURA A.
; APPLICANT: REJTO, PAUL A.
; APPLICANT: SHOWALTER, RICHARD E.
; APPLICANT: TEMPICZYK-RUSSELL, ANNA
; APPLICANT: THOMSON, JIM
; APPLICANT: VANDERPOOL, DARTIN
; APPLICANT: VILLAFRANCA, J. ERNEST
; TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
; TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
; FILE REFERENCE: 0125-0049
; CURRENT APPLICATION NUMBER: US/09/931.186
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: full length mutant ERAB C214R
US-09-931-186-2
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Query Match 99.1%; Score 1297; DB 10; Length 261;

Best Local Similarity 99.6%; Pred. No. 6.7e-110;

Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MAACRSYKGLVAVYITGASGLGATPARELVGQASAVLDELPSGSGEAKKRGNNCF 60
Db 1 MAACRSYKGLVAVYITGASGLGATPARELVGQASAVLDELPSGSGEAKKRGNNCF 60
QY 61 APADVTSEEDVOTALALAKGKGRVDVAVNCAAGINAVASTYLNKKQCTHTLDDPQAVLDV 120
Db 61 APADVTSEEDVOTALALAKGKGRVDVAVNCAAGINAVASTYLNKKQCTHTLDDPQAVLDV 120
QY 121 NMGTENVIRLVAGENGQNEPDGGGQGVYINTASVAEFGVGQAAYASASGKGYGML 180
Db 121 NMGTENVIRLVAGENGQNEPDGGGQGVYINTASVAEFGVGQAAYASASGKGYGML 180
QY 181 PIARDLAPIGIRVMTLAPGFGFPLTSLPEKVCNPLASQVPPPSRLGDPAEYAHLYQAI 240
Db 181 PIARDLAPIGIRVMTLAPGFGFPLTSLPEKVCNPLASQVPPPSRLGDPAEYAHLYQAI 240
QY 241 IENPFLNGEVIRLDGAIKMQP 261
Db 241 IENPFLNGEVIRLDGAIKMQP 261
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RESULT 7

```
US-09-984-245-245
; Sequence 245, Application US/09984245
; Patent No. US20020165374A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/984.245
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 245
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-245-245
```

Query Match

87.5%; Score 1146; DB 9; Length 227;

APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
TITLE OF INVENTION: OF INHIBITORS THEREOF
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C5V
US-09-931-186-4

Query Match 99.2%; Score 1299; DB 10; Length 261;
Best Local Similarity 99.6%; Pred. No. 4.4e-110;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAACRSYKGLVAVITGASGLGATAEERLVGGASAVLLDLPNSGGEAQAQKLGNNCYF 60
DB 1 MAAAVRSYKGLVAVITGASGLGATAEERLVGGASAVLLDLPNSGGEAQAQKLGNNCYF 60
QY 61 APADVTSEKDVOTATLAKKFGFRVDVAVNACGIAVASKTYNLKKGQTHLEDFQRYLDV 120
DB 61 APADVTSEKDVOTATLAKKFGFRVDVAVNACGIAVASKTYNLKKGQTHLEDFQRYLDV 120
QY 121 NLGTFNVIRLVAGEMQNEPDGQGVIIINTASVAAEFGVGOAAYSASKGIWMTL 180
DB 121 NLGTFNVIRLVAGEMQNEPDGQGVIIINTASVAAEFGVGOAAYSASKGIWMTL 180
QY 181 PIARDLAPIGIRVMTAPGLFTPLTSLPEKVCNFLASQVPPPSRLGDAPEYAHLYOAI 240
DB 181 PIARDLAPIGIRVMTAPGLFTPLTSLPEKVCNFLASQVPPPSRLGDAPEYAHLYOAI 240
QY 241 IENPFLNGEVIRLDGAIKMP 261
DB 241 IENPFLNGEVIRLDGAIKMP 261

RESULT 4
US-09-931-186-6
Sequence 6, Application US/09931186
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABREO, MELWYN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPCZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
TITLE OF INVENTION: OF INHIBITORS THEREOF
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 261
TYPE: PRT

ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C58V
US-09-931-186-6

Query Match 99.2%; Score 1299; DB 10; Length 261;
Best Local Similarity 99.6%; Pred. No. 4.4e-110;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 181 PIARDLAPIGIRVMTAPGLFTPLTSLPEKVCNFLASQVPPPSRLGDAPEYAHLYOAI 240
QY 241 IENPFLNGEVIRLDGAIKMP 261
DB 241 IENPFLNGEVIRLDGAIKMP 261

RESULT 5
US-09-931-186-23
Sequence 23, Application US/09931186
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABREO, MELWYN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPCZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
TITLE OF INVENTION: OF INHIBITORS THEREOF
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C214S
US-09-931-186-23

Query Match 99.2%; Score 1299; DB 10; Length 261;
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53 233 17.8 311 9 US-09-738-626-3819 Sequence 3819, Ap
94 231 17.6 261 10 US-09-815-242-5813 Sequence 5813, Ap
95 225.5 17.2 247 10 US-09-815-242-11342 Sequence 11342, A
96 224 17.1 254 10 US-09-741-669-411 Sequence 411, App
97 222.5 17.0 247 10 US-09-815-242-11514 Sequence 11514, A
98 222.5 17.0 900 9 US-10-060-230-15 Sequence 15, Appl
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ALIGNMENTS

RESULT 1
US-09-931-186-8
Sequence 8, Application US/09931186
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABREO, MELWYN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPICZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 261
TYPE: PR1
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: wild type ERAB
US-09-931-186-8

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Best Local Similarity 100.0%; Pred. No. 5.4e-111;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 241 IENPFLNGEVIIRLDGAIKMP 261

RESULT 2

US-09-931-186-20
Sequence 20, Application US/09931186
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABREO, MELWYN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPICZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 261
TYPE: PR1
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C214A
US-09-931-186-20

Query Match 99.3%; Score 1300; DB 10; Length 261;
Best Local Similarity 99.6%; Pred. No. 3.6e-110;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 241 IENPFLNGEVIIRLDGAIKMP 261

RESULT 3
US-09-931-186-4
Sequence 4, Application US/09931186
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABREO, MELWYN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPICZYK-RUSSELL, ANNA

Thu Jun 26 06:55:11 2003

us-09-931-186-8.rapb

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:32:58 ; Search time 20.333 Seconds

(Without alignments)
1388.950 Million cell updates/sec

Title: US-09-931-186-8

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Searched: 417779 segs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

Published Applications AA: *
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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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56	285.5	21.8	244	9	US-10-175-696-19
57	283.5	21.7	203	10	US-09-823-901-7
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C:Genetics:

A:Gene: fadG

A:Map position: linear chromosome

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match

Best Local Similarity

Matches

94; Conservative

44; Mismatches

91; Indels

31; Gaps

10;

24.0%; Score 314.5; DB 2; Length 259;

36.2%; Pred. No. 1.8e-17;

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QY 238 QAIEN--PFLNGEYIRLDG 255

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